FIG. 1A

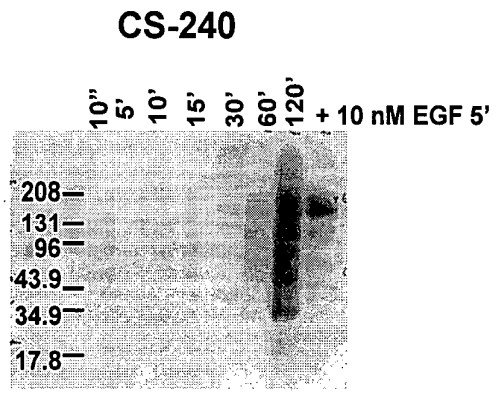
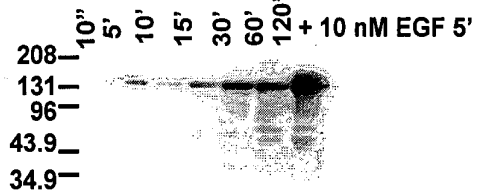
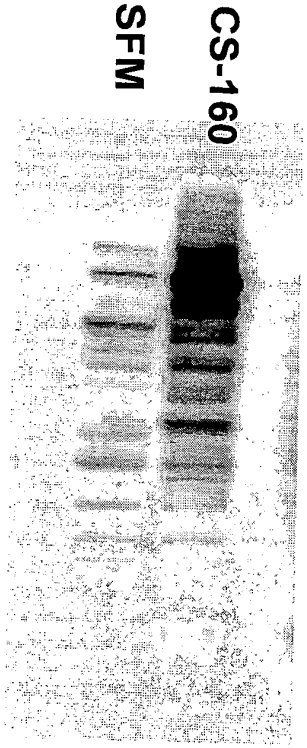


FIG. 1B



CS240 = 240 cigarettes/ 500 ml RPMI = ~ 5 cigarettes/ 10 ml

FIG. 2A



Whole cell lysate
Without Immunoprecipitation

FIG. 2B

Whole Cell Lysate
Immunoprecipitation for Phosphotyrosine

FIG. 3

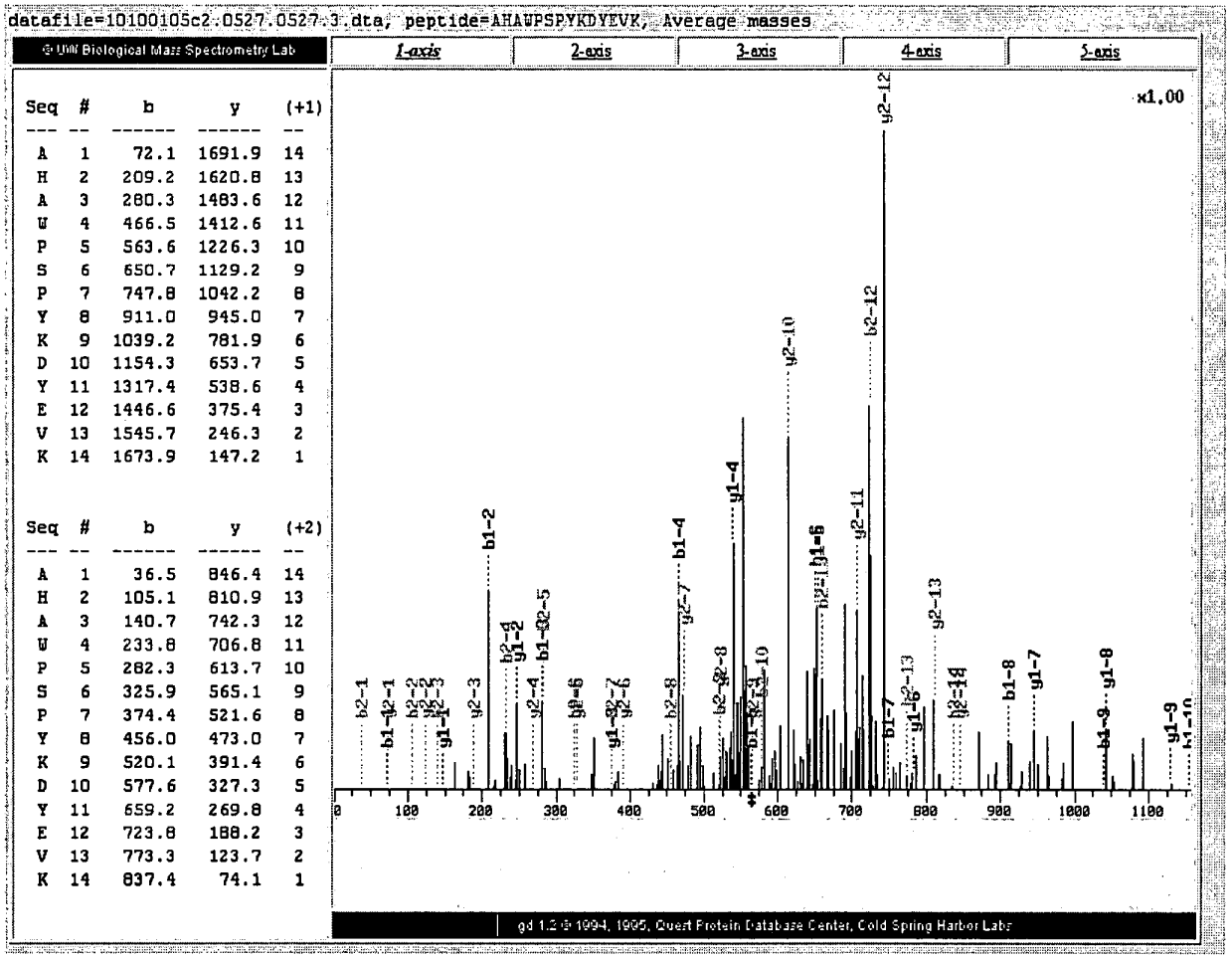

datafile=101001105c2.0527.0527.3.dta, peptide=AHAWPSPYKDYEVK, Average masses
© UW Biological Mass Spectrometry Lab
1-axis
2-axis
3-axis
4-axis
5-axis
x1.00
Seq # b y (+1)
A 1 72.1 1691.9 14
H 2 209.2 1620.8 13
A 3 280.3 1483.6 12
W 4 466.5 1412.6 11
P 5 563.6 1226.3 10
S 6 650.7 1129.2 9
P 7 747.8 1042.2 8
Y 8 911.0 945.0 7
K 9 1039.2 781.9 6
D 10 1154.3 653.7 5
Y 11 1317.4 538.6 4
E 12 1446.6 375.4 3
V 13 1545.7 246.3 2
K 14 1673.9 147.2 1
Seq # b y (+2)
A 1 36.5 846.4 14
H 2 105.1 810.9 13
A 3 140.7 742.3 12
W 4 233.8 706.8 11
P 5 282.3 613.7 10
S 6 325.9 565.1 9
P 7 374.4 521.6 8
Y 8 456.0 473.0 7
K 9 520.1 391.4 6
D 10 577.6 327.3 5
Y 11 659.2 269.8 4
E 12 723.8 188.2 3
V 13 773.3 123.7 2
K 14 837.4 74.1 1
0
100
200
300
400
500
600
700
800
900
1000
1100
gd 1.2 © 1994, 1995, Quest Protein Database Center, Cold Spring Harbor Labs

FIG. 4

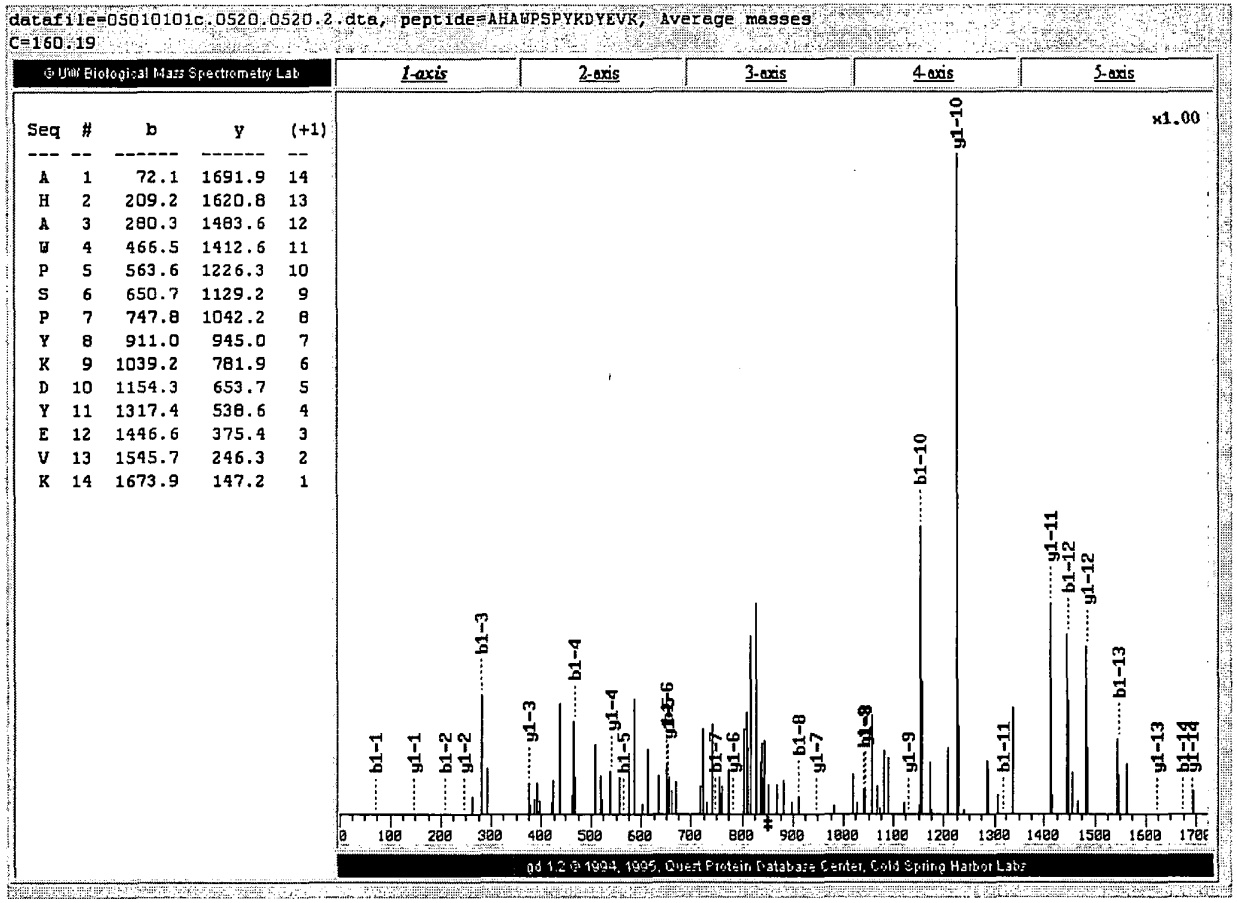

datafile=05010101c.0520.0520.2.dta, peptide=AHAWPSPYKDYEVK, Average masses
C=160.19
© UWI Biological Mass Spectrometry Lab
1-axis
2-axis
3-axis
4-axis
5-axis
Seq # b y (+1)
A 1 72.1 1691.9 14
H 2 209.2 1620.8 13
A 3 280.3 1483.6 12
W 4 466.5 1412.6 11
P 5 563.6 1226.3 10
S 6 650.7 1129.2 9
P 7 747.8 1042.2 8
Y 8 911.0 945.0 7
K 9 1039.2 781.9 6
D 10 1154.3 653.7 5
Y 11 1317.4 538.6 4
E 12 1446.6 375.4 3
V 13 1545.7 246.3 2
K 14 1673.9 147.2 1
x1.00
b1-1
y1-1
b1-2
y1-2
b1-3
y1-3
b1-4
y1-4
b1-5
y1-5
b1-6
y1-6
b1-7
y1-7
b1-8
y1-8
b1-9
y1-9
b1-10
y1-10
b1-11
y1-11
b1-12
y1-12
b1-13
y1-13
b1-14
y1-14
0 100 200 300 400 500 600 700 800 900 1000 1100 1200 1300 1400 1500 1600 1700
gd 1.2 © 1994, 1995, Quest Protein Database Center, Cold Spring Harbor Labs

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FIG. 5

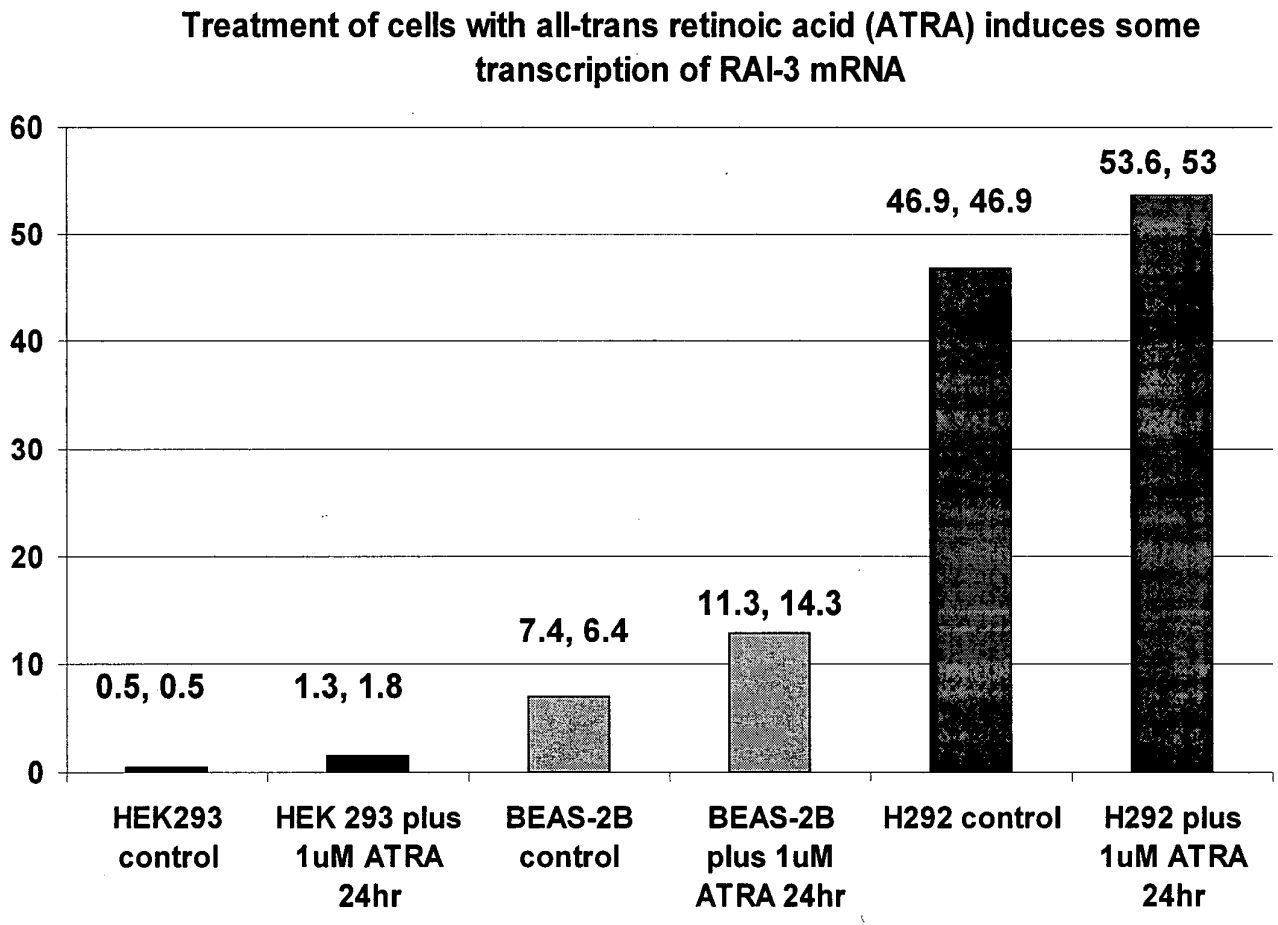

Treatment of cells with all-trans retinoic acid (ATRA) induces some transcription of RAI-3 mRNA
60
50
40
30
20
10
0
0.5, 0.5
1.3, 1.8
7.4, 6.4
11.3, 14.3
46.9, 46.9
53.6, 53
HEK293 control
HEK 293 plus 1uM ATRA 24hr
BEAS-2B control
BEAS-2B plus 1uM ATRA 24hr
H292 control
H292 plus 1uM ATRA 24hr

FIG. 6

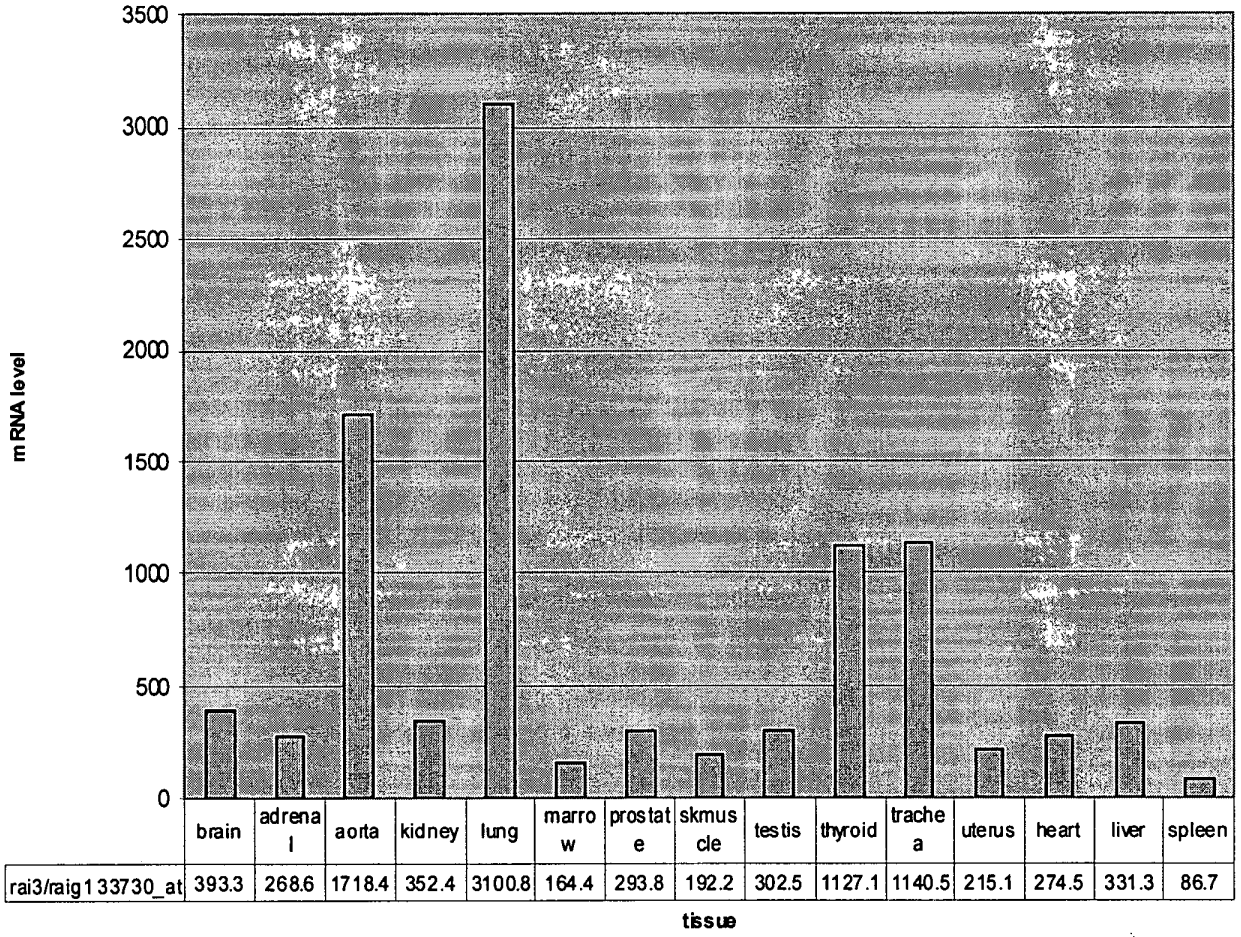

3500
3000
2500
2000
1500
1000
500
0
mRNA level
brain
adrenal
aorta
kidney
lung
marrow
prostate
skmuscle
testis
thyroid
trachea
uterus
heart
liver
spleen
rai3/raig1 33730_at
393.3
268.6
1718.4
352.4
3100.8
164.4
293.8
192.2
302.5
1127.1
1140.5
215.1
274.5
331.3
86.7
tissue

FIG. 7

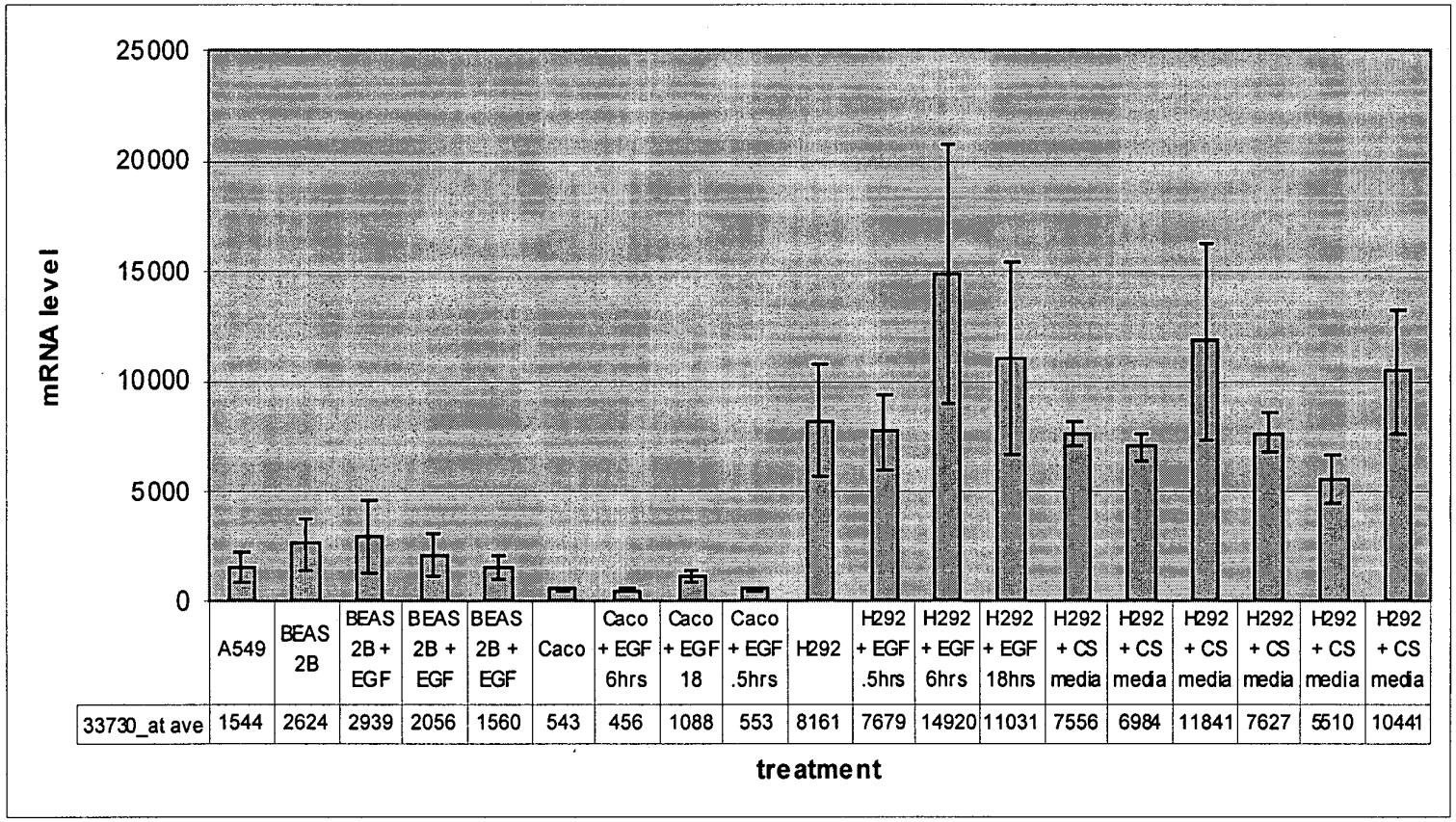
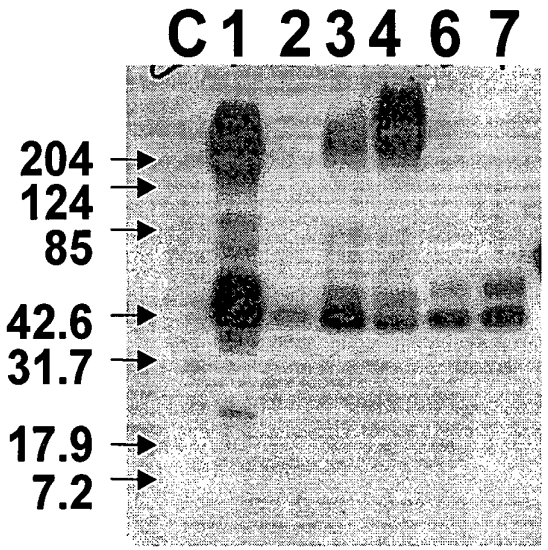
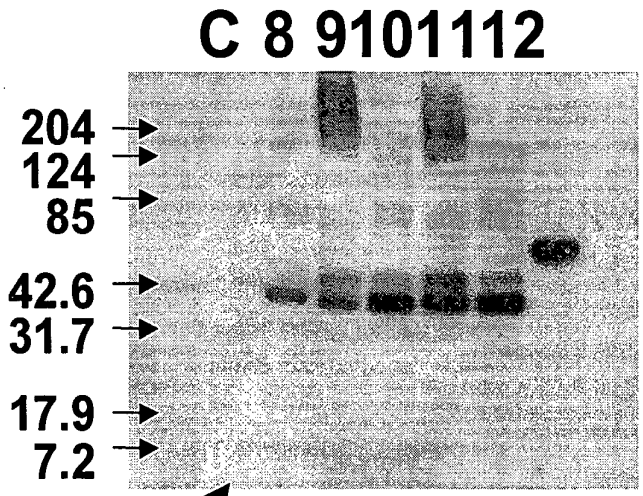

25000
20000
15000
10000
5000
0
mRNA level
A549
BEAS 2B
BEAS 2B + EGF
BEAS 2B + EGF
BEAS 2B + EGF
Caco
Caco + EGF 6hrs
Caco + EGF 18
Caco + EGF .5hrs
H292
H292 + EGF .5hrs
H292 + EGF 6hrs
H292 + EGF 18hrs
H292 + CS media
H292 + CS media
H292 + CS media
H292 + CS media
H292 + CS media
H292 + CS media
33730_at ave
1544
2624
2939
2056
1560
543
456
1088
553
8161
7679
14920
11031
7556
6984
11841
7627
5510
10441
treatment

FIG. 8A



Control untransfected HEK 293 cells

FIG. 8B



Control FLAG-fusion protein 52/48 kD

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FIG. 9A

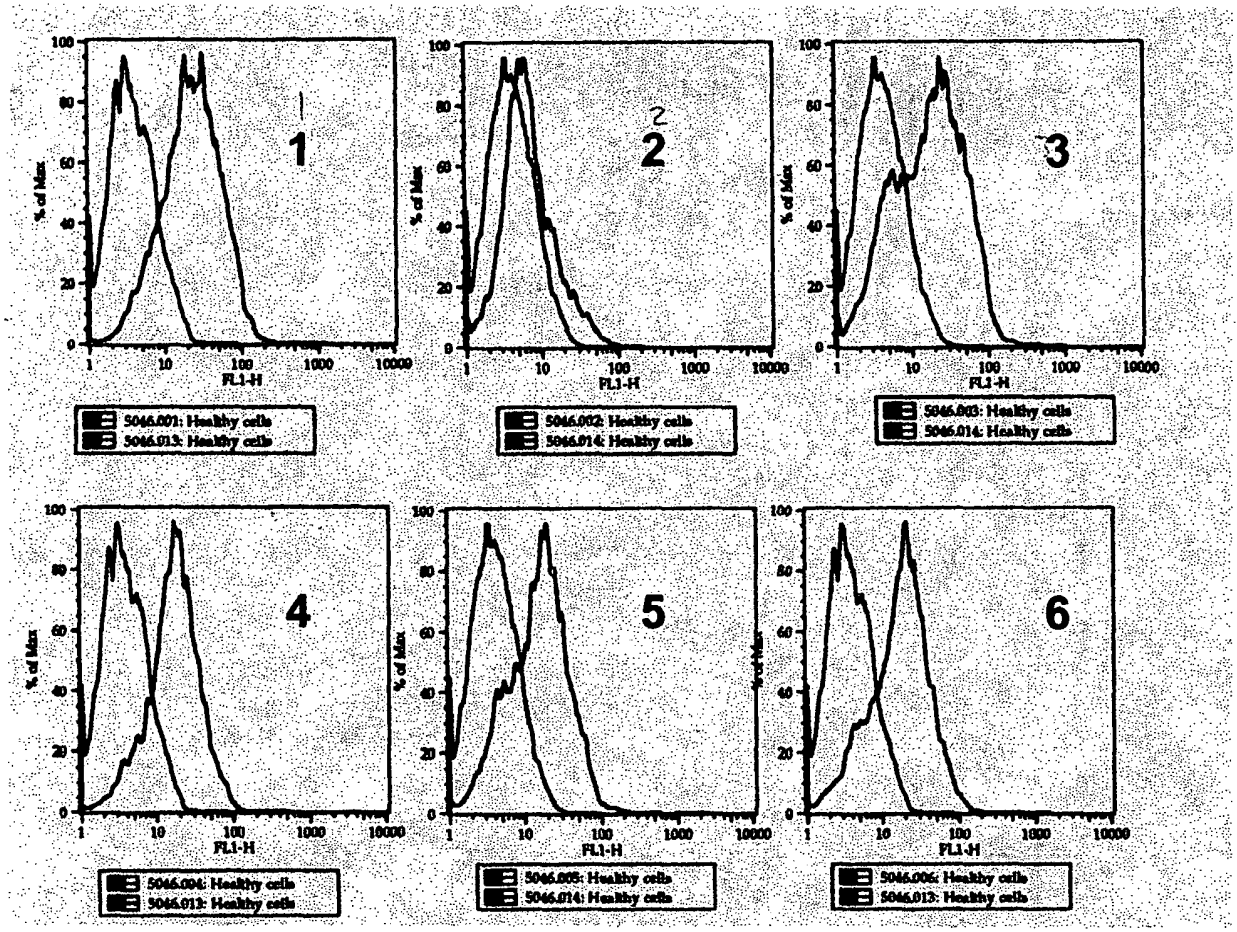

1
2
3
4
5
6
% of Max
FL1-H
5046.001: Healthy cells
5046.013: Healthy cells
5046.002: Healthy cells
5046.014: Healthy cells
5046.003: Healthy cells
5046.014: Healthy cells
5046.004: Healthy cells
5046.013: Healthy cells
5046.005: Healthy cells
5046.014: Healthy cells
5046.006: Healthy cells
5046.013: Healthy cells

FIG. 9B

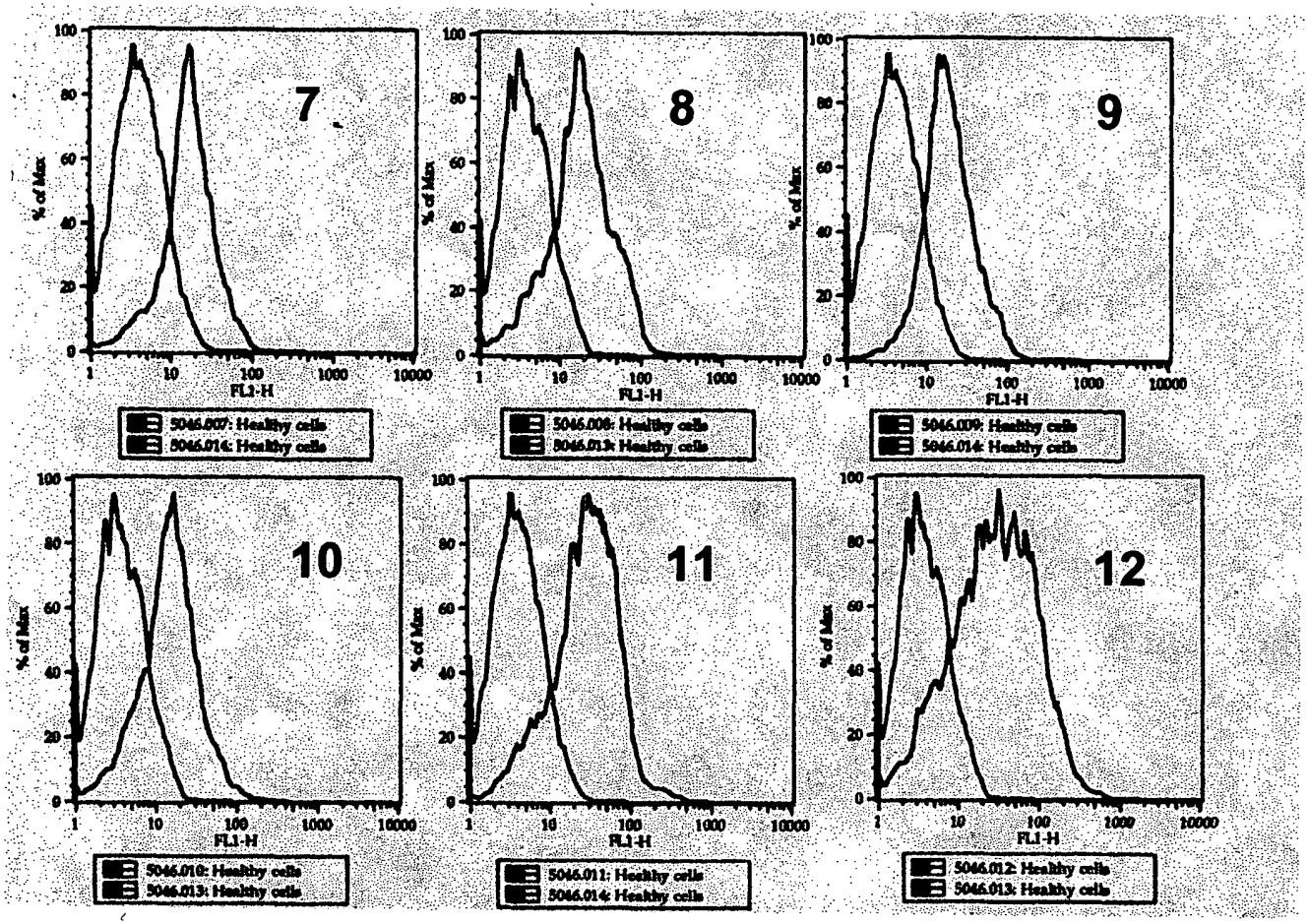

7
8
9
10
11
12
% of Max
FL1-H
5046.007: Healthy cells
5046.014: Healthy cells
5046.008: Healthy cells
5046.013: Healthy cells
5046.009: Healthy cells
5046.014: Healthy cells
5046.010: Healthy cells
5046.013: Healthy cells
5046.011: Healthy cells
5046.014: Healthy cells
5046.012: Healthy cells
5046.013: Healthy cells

FIG. 10A

```
   1 ataacagcat gaagtgccgt ggaactggaa taggcgtgtc ctctccctcg accctccccc
  61 tccttgtccc tctgctcacc cctcgctcgt tccctccctc cggcgagggc cgcctttata
 121 acaactgctc agagtgcgag ggcgggatag ctgtccaagg tctcccccag cactgaggag
 181 ctcgcctgct gccctcttgc gcgcgggaag cagcaccaag ttcacggcca acgccttggc
 241 actagggtcc agaatggcta caacagtccc tgatggttgc cgcaatggcc tgaaatccaa
 301 gtactacaga ctttgtgata aggctgaagc ttggggcatc gtcctagaaa cggtggccac
 361 agccggggtt gtgacctcgg tggccttcat gctcactctc ccgatcctcg tctgcaaggt
 421 gcaggactcc aacaggcgaa aaatgctgcc tactcagttt ctcttcctcc tgggtgtgtt
 481 gggcatcttt ggcctcacct tcgccttcat catcggactg gacgggagca cagggcccac
 541 acgcttcttc ctctttggga tcctcttttc catctgcttc tcctgcctgc tggctcatgc
 601 tgtcagtctg accaagctcg tccgggggag gaagcccctt tccctgttgg tgattctggg
 661 tctggccgtg ggcttcagcc tagtccagga tgttatcgct attgaatata ttgtcctgac
 721 catgaatagg accaacgtca atgtcttttc tgagctttcc gctcctcgtc gcaatgaaga
 781 ctttgtcctc ctgctcacct acgtcctctt cttgatggcg ctgaccttcc tcatgtcctc
 841 cttcaccttc tgtggttcct tcacgggctg gaagagacat ggggcccaca tctacctcac
 901 gatgctcctc tccattgcca tctgggtggc ctggatcacc ctgctcatgc ttcctgactt
 961 tgaccgcagg tgggatgaca ccatcctcag ctccgccttg gctgccaatg gctgggtgtt
1021 cctgttggct tatgttagtc ccgagttttg gctgctcaca aagcaacgaa accccatgga
1081 ttatcctgtt gaggatgctt tctgtaaacc tcaactcgtg aagaagagct atggtgtgga
1141 gaacagagcc tactctcaag aggaaatcac tcaaggtttt gaagagacag gggacacgct
1201 ctatgccccc tattccacac attttcagct gcagaaccag cctccccaaa aggaattctc
1261 catcccacgg gcccacgctt ggccgagccc ttacaaagac tatgaagtaa agaaagaggg
1321 cagctaactc tgtcctgaag agtgggacaa atgcagccgg gcggcagatc tagcgggagc
1381 tcaaagggat gtgggcgaaa tcttgagtct tctgagaaaa ctgtacaaga cactacggga
1441 acagtttgcc tccctcccag cctcaaccac aattcttcca tgctggggct gatgtgggct
1501 agtaagactc cagttcttag aggcgctgta gtatttttt ttttttgtct catcctttgg
1561 atacttcttt taagtgggag tctcaggcaa ctcaagttta gacccttact ctttttgttt
1621 gtttttttgaa acaggatctt gctctgtcac ccaggcttga gtgcagtggt gcgatcacag
1681 cccagtgcag cctcgaccac ctgtgctcaa gcaatcctcc catctccatc tcccaaagtg
1741 ctgggatgac aggcgtgagc cacagctccc agcctaggcc cttaatcttg ctgttatttt
1801 ccatggacta aaggtctggt catctgagct cacgctggct cacacagctc taggggcctg
1861 ctcctctaac tcacagtggg ttttgtgagg ctctgtggcc cagagcagac ctgcatatct
1921 gagcaaaaat agcaaaagcc tctctcagcc cactggcctg aatctacact ggaagccaac
1981 ttgctggcac ccccgctccc caacccttct tgcctgggta ggagaggcta aagatcaccc
2041 taaatttact catctctcta gtgctgcctc acattgggcc tcagcagctc cccagcacca
```

FIG. 10B

```
2101 attcacaggt cacccctctc ttcttgcact gtccccaaac ttgctgtcaa ttccgagatc
2161 taatctcccc ctacgctctg ccaggaattc tttcagacct cactagcaca agcccggttg
2221 ctccttgtca ggagaatttg tagatcattc tcacttcaaa ttcctggggc tgatacttct
2281 ctcatcttgc accccaacct ctgtaaatag atttaccgca tttacggctg cattctgtaa
2341 gtgggcatgg tctcctaatg gaggagtgtt cattgtataa taagttattc acctgagtat
2401 gcaataaaga tgtggtggcc actctttcat ggtggtggca gcaaaaaaaa aaaaaa
```

FIG. 11A

```
  1 MATTVPDGCR NGLKSKYYRL CDKAEAWGIV LETVATAGVV TSVAFMLTLP ILVCKVQDSN
 61 RRKMLPTQFL FLLGVLGIFG LTFAFIIGLD GSTGPTRFFL FGILFSICFS CLLAHAVSLT
121 KLVRGRKPLS LLVILGLAVG FSLVQDVIAI EYIVLTMNRT NVNVFSELSA PRRNEDFVLL
181 LTYVLFLMAL TFLMSSFTFC GSFTGWKRHG AHIYLTMLLS IAIWVAWITL LMLPDFDRRW
241 DDTILSSALA ANGWVFLLAY VSPEFWLLTK QRNPMDYPVE DAFCKPQLVK KSYGVENRAY
301 SQEEITQGFE ETGDTLYAPY STHFQLQNQP PQKEFSIPRA HAWPSPYKDY EVKKEGS
```

FIG. 11B

```
   1  ataacagcatgaagtgccgtggaactggaataggcgtgtcctctccctcgaccctccccc    60

  61  tccttgtccctctgctcacccctcgctcgttccctccctccggcgagggccgcctttata   120

 121  acaactgctcagagtgcgagggcgggatagctgtccaaggtctcccccagcactgaggag   180

 181  ctcgcctgctgccctcttgcgcgcgggaagcagcaccaagttcacggccaacgccttggc   240

 241  actagggtccagaatggctacaacagtccctgatggttgccgcaatggcctgaaatccaa   300
   1                  M  A  T  T  V  P  D  G  C  R  N  G  L  K  S  K    16

 301  gtactacagactttgtgataaggctgaagcttggggcatcgtcctagaaacggtggccac   360
  17   Y  Y  R  L  C  D  K  A  E  A  W  G  I  V  L  E  T  V  A  T    36

 361  agccggggttgtgacctcggtggccttcatgctcactctcccgatcctcgtctgcaaggt   420
  37   A  G  V  V  T  S  V  A  F  M  L  T  L  P  I  L  V  C  K  V    56

 421  gcaggactccaacaggcgaaaaatgctgcctactcagtttctcttcctcctgggtgtgtt   480
  57   Q  D  S  N  R  R  K  M  L  P  T  Q  F  L  F  L  L  G  V  L    76

 481  gggcatctttggcctcaccttcgccttcatcatcggactggacgggagcacagggcccac   540
  77   G  I  F  G  L  T  F  A  F  I  I  G  L  D  G  S  T  G  P  T    96

 541  acgcttcttcctctttgggatcctcttttccatctgcttctcctgcctgctggctcatgc   600
  97   R  F  F  L  F  G  I  L  F  S  I  C  F  S  C  L  L  A  H  A   116

 601  tgtcagtctgaccaagctcgtccgggggaggaagccccttccctgttggtgattctggg   660
 117   V  S  L  T  K  L  V  R  G  R  K  P  L  S  L  L  V  I  L  G   136

 661  tctggccgtgggcttcagcctagtccaggatgttatcgctattgaatatattgtcctgac   720
 137   L  A  V  G  F  S  L  V  Q  D  V  I  A  I  E  Y  I  V  L  T   156

 721  catgaataggaccaacgtcaatgtcttttctgagctttccgctcctcgtcgcaatgaaga   780
 157   M  N  R  T  N  V  N  V  F  S  E  L  S  A  P  R  R  N  E  D   176

 781  ctttgtcctcctgctcacctacgtcctcttcttgatggcgctgaccttcctcatgtcctc   840
 177   F  V  L  L  L  T  Y  V  L  F  L  M  A  L  T  F  L  M  S  S   196

 841  cttcaccttctgtggttccttcacgggctggaagagacatggggcccacatctacctcac   900
 197   F  T  F  C  G  S  F  T  G  W  K  R  H  G  A  H  I  Y  L  T   216

 901  gatgctcctctccattgccatctgggtggcctggatcaccctgctcatgcttcctgactt   960
 217   M  L  L  S  I  A  I  W  V  A  W  I  T  L  L  M  L  P  D  F   236

 961  tgaccgcaggtgggatgacaccatcctcagctccgccttggctgccaatggctgggtgtt  1020
 237   D  R  R  W  D  D  T  I  L  S  S  A  L  A  A  N  G  W  V  F   256

1021  cctgttggcttatgttagtcccgagttttggctgctcacaaagcaacgaaaccccatgga  1080
 257   L  L  A  Y  V  S  P  E  F  W  L  L  T  K  Q  R  N  P  M  D   276

1081  ttatcctgttgaggatgctttctgtaaacctcaactcgtgaagaagagctatggtgtgga  1140
 277   Y  P  V  E  D  A  F  C  K  P  Q  L  V  K  K  S  Y  G  V  E   296

1141  gaacagagcctactctcaagaggaaatcactcaaggttttgaagagacaggggacacgct  1200
 297   N  R  A  Y  S  Q  E  E  I  T  Q  G  F  E  E  T  G  D  T  L   316
```

FIG. 11C

```
1201 ctatgccccctattccacacattttcagctgcagaaccagcctccccaaaaggaattctc   1260
317   Y  A  P  Y  S  T  H  F  Q  L  Q  N  Q  P  P  Q  K  E  F  S    336

1261 catcccacgggcccacgcttggccgagcccttacaaagactatgaagtaaagaaagaggg   1320
337   I  P  R  A  H  A  W  P  S  P  Y  K  D  Y  E  V  K  K  E  G    356

1321 cagctaactctgtcctgaagagtgggacaaatgcagccgggcggcagatctagcgggagc   1380
357   S                                                             357

1381  tcaaagggatgtgggcgaaatcttgagtcttctgagaaaactgtacaagacactacggga   1440

1441  acagtttgcctccctcccagcctcaaccacaattcttccatgctggggctgatgtgggct   1500

1501  agtaagactccagttcttagaggcgctgtagtatttttttttttttgtctcatcctttgg   1560

1561  atacttcttttaagtgggagtctcaggcaactcaagtttagacccttactctttttgttt   1620

1621  gtttttgaaacaggatcttgctctgtcacccaggcttgagtgcagtggtgcgatcacag   1680

1681  cccagtgcagcctcgaccacctgtgctcaagcaatcctcccatctccatctcccaaagtg   1740

1741  ctgggatgacaggcgtgagccacagctcccagcctaggcccttaatcttgctgttatttt   1800

1801  ccatggactaaaggtctggtcatctgagctcacgctggctcacacagctctaggggcctg   1860

1861  ctcctctaactcacagtgggttttgtgaggctctgtggcccagagcagacctgcatatct   1920

1921  gagcaaaaatagcaaaagcctctctcagcccactggcctgaatctacactggaagccaac   1980

1981  ttgctggcacccccgctccccaacccttcttgcctgggtaggagaggctaaagatcaccc   2040

2041  taaatttactcatctctctagtgctgcctcacattgggcctcagcagctccccagcacca   2100

2101  attcacaggtcacccctctcttcttgcactgtccccaaacttgctgtcaattccgagatc   2160

2161  taatctccccctacgctctgccaggaattctttcagacctcactagcacaagcccggttg   2220

2221  ctccttgtcaggagaatttgtagatcattctcacttcaaattcctggggctgatacttct   2280

2281  ctcatcttgcaccccaacctctgtaaatagatttaccgcatttacggctgcattctgtaa   2340

2341  gtgggcatggtctcctaatggaggagtgttcattgtataataagttattcacctgagtat   2400

2401  gcaataaagatgtggtggccactctttcatggtggtggcagcaaaaaaaaaaaaaa  2456
```

FIG. 12

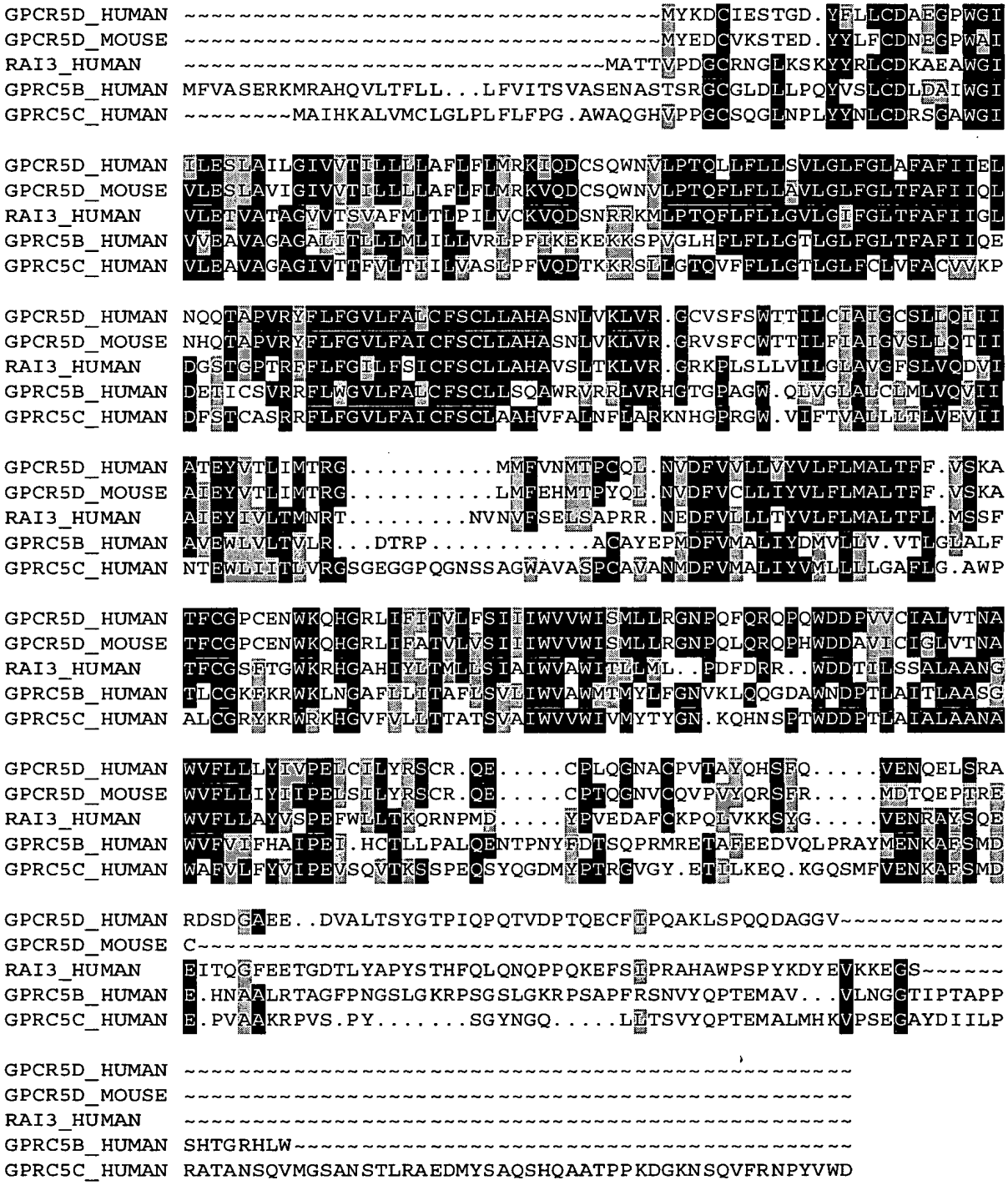

GPCR5D_HUMAN
GPCR5D_MOUSE
RAI3_HUMAN
GPRC5B_HUMAN
GPRC5C_HUMAN

FIG. 13

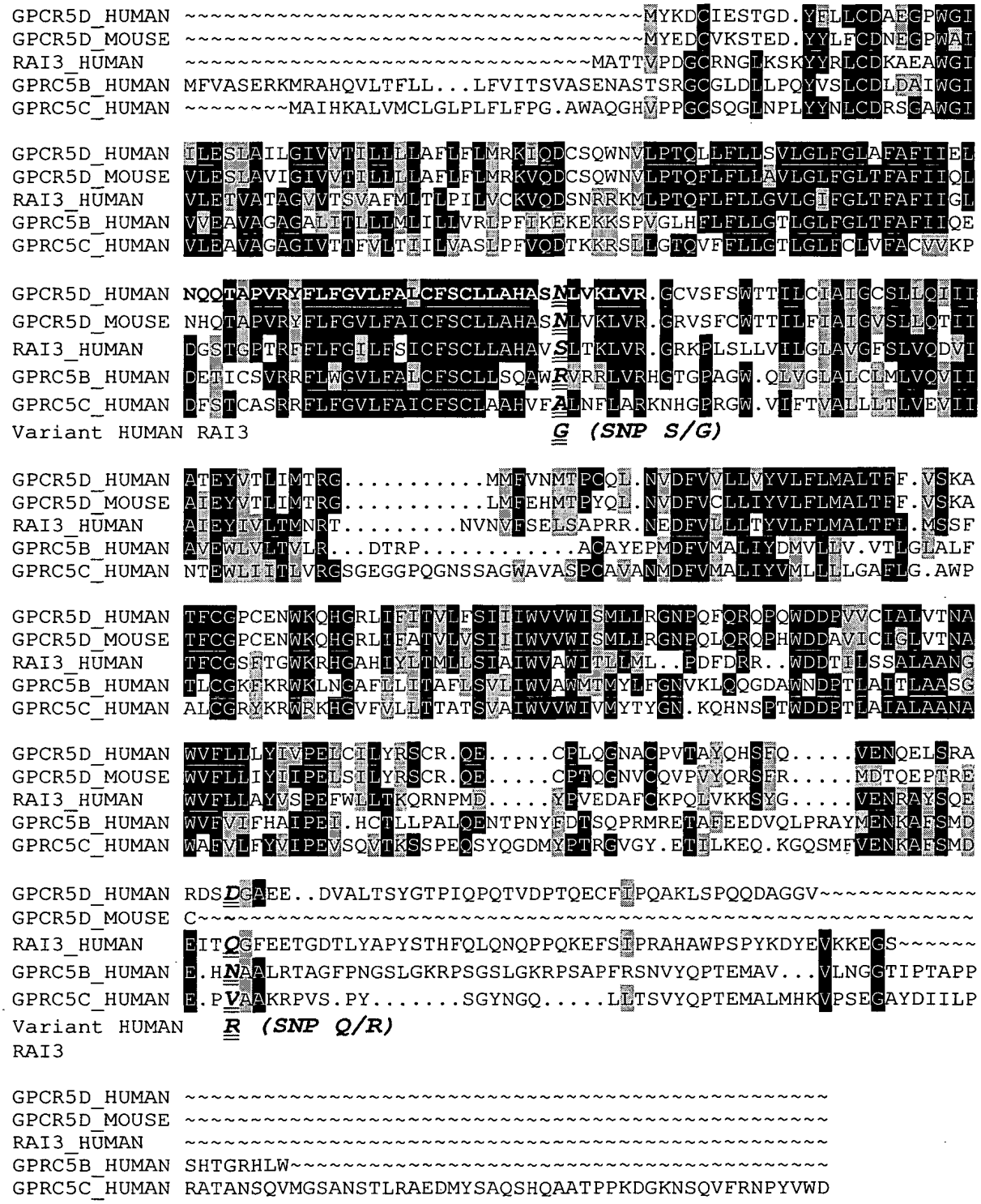

GPCR5D_HUMAN
GPCR5D_MOUSE
RAI3_HUMAN
GPRC5B_HUMAN
GPRC5C_HUMAN
Variant HUMAN RAI3
G (SNP S/G)
R (SNP Q/R)
RAI3

FIG. 14A

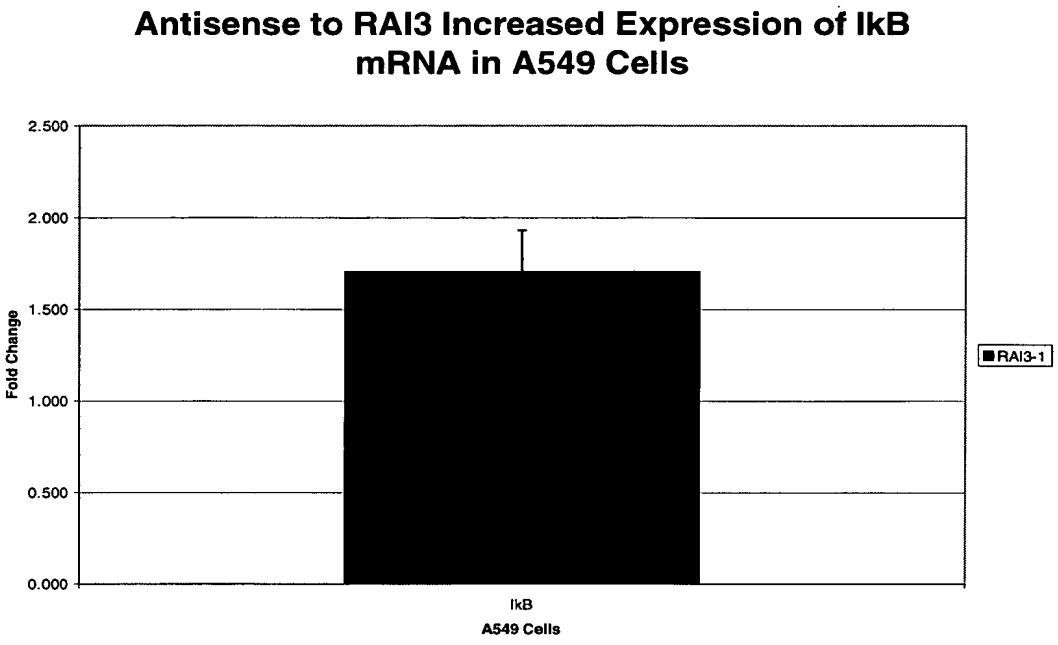

Antisense to RAI3 Increased Expression of IkB mRNA in A549 Cells
2.500
2.000
1.500
1.000
0.500
0.000
Fold Change
IkB
A549 Cells
RAI3-1

FIG. 14B

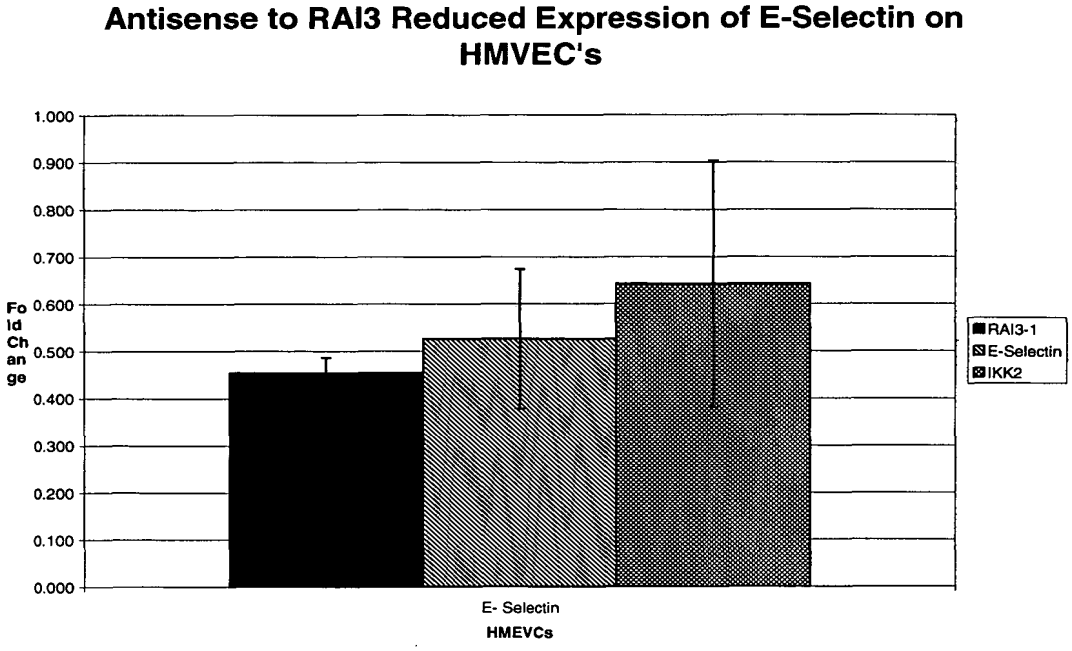

Antisense to RAI3 Reduced Expression of E-Selectin on HMVEC's
1.000
0.900
0.800
0.700
0.600
0.500
0.400
0.300
0.200
0.100
0.000
Fold Change
E- Selectin
HMEVCs
RAI3-1
E-Selectin
IKK2

FIG. 15

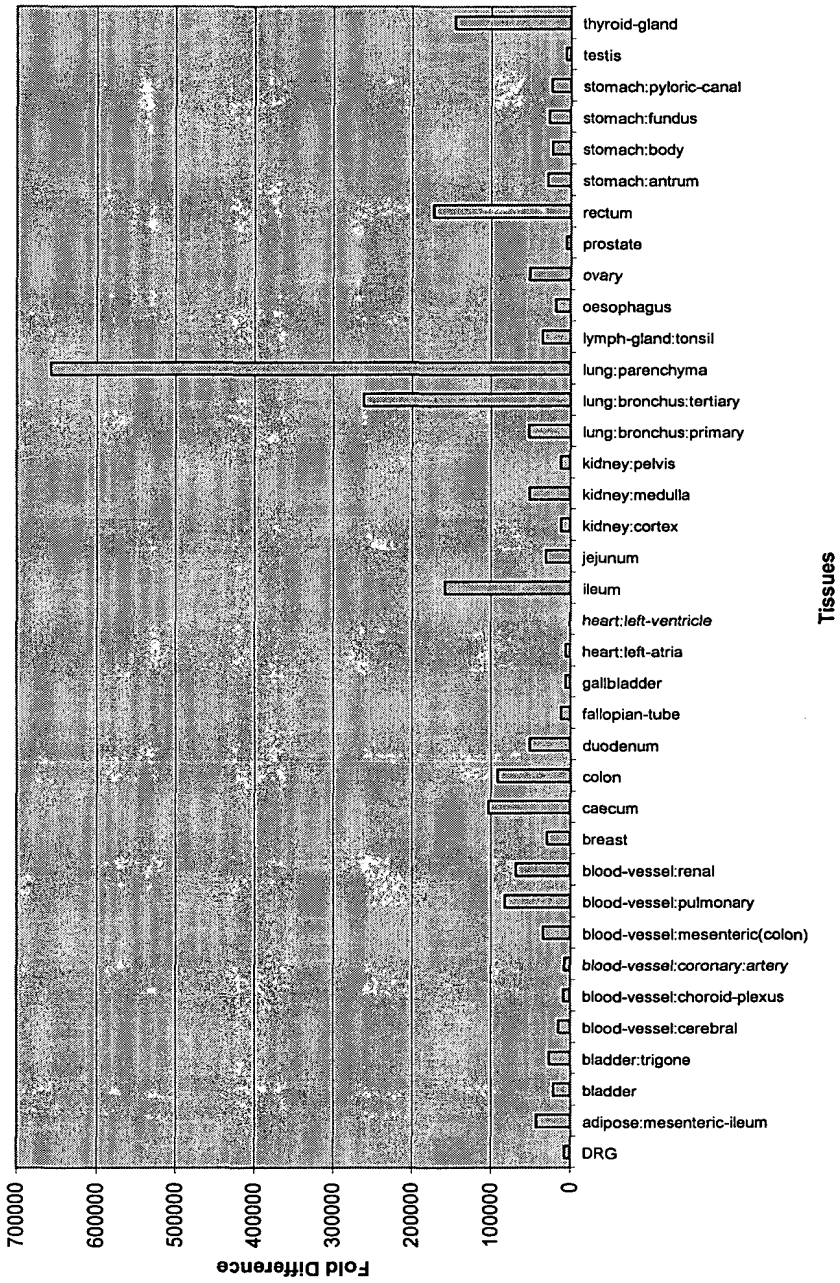

RAI-3 Relative Expression in normal Tissue RNAs
Fold Difference
0
100000
200000
300000
400000
500000
600000
700000
Tissues
thyroid-gland
testis
stomach:pyloric-canal
stomach:fundus
stomach:body
stomach:antrum
rectum
prostate
ovary
oesophagus
lymph-gland:tonsil
lung:parenchyma
lung:bronchus:tertiary
lung:bronchus:primary
kidney:pelvis
kidney:medulla
kidney:cortex
jejunum
ileum
heart:left-ventricle
heart:left-atria
gallbladder
fallopian-tube
duodenum
colon
caecum
breast
blood-vessel:renal
blood-vessel:pulmonary
blood-vessel:mesenteric(colon)
blood-vessel:coronary:artery
blood-vessel:choroid-plexus
blood-vessel:cerebral
bladder:trigone
bladder
adipose:mesenteric-ileum
DRG

FIG. 16

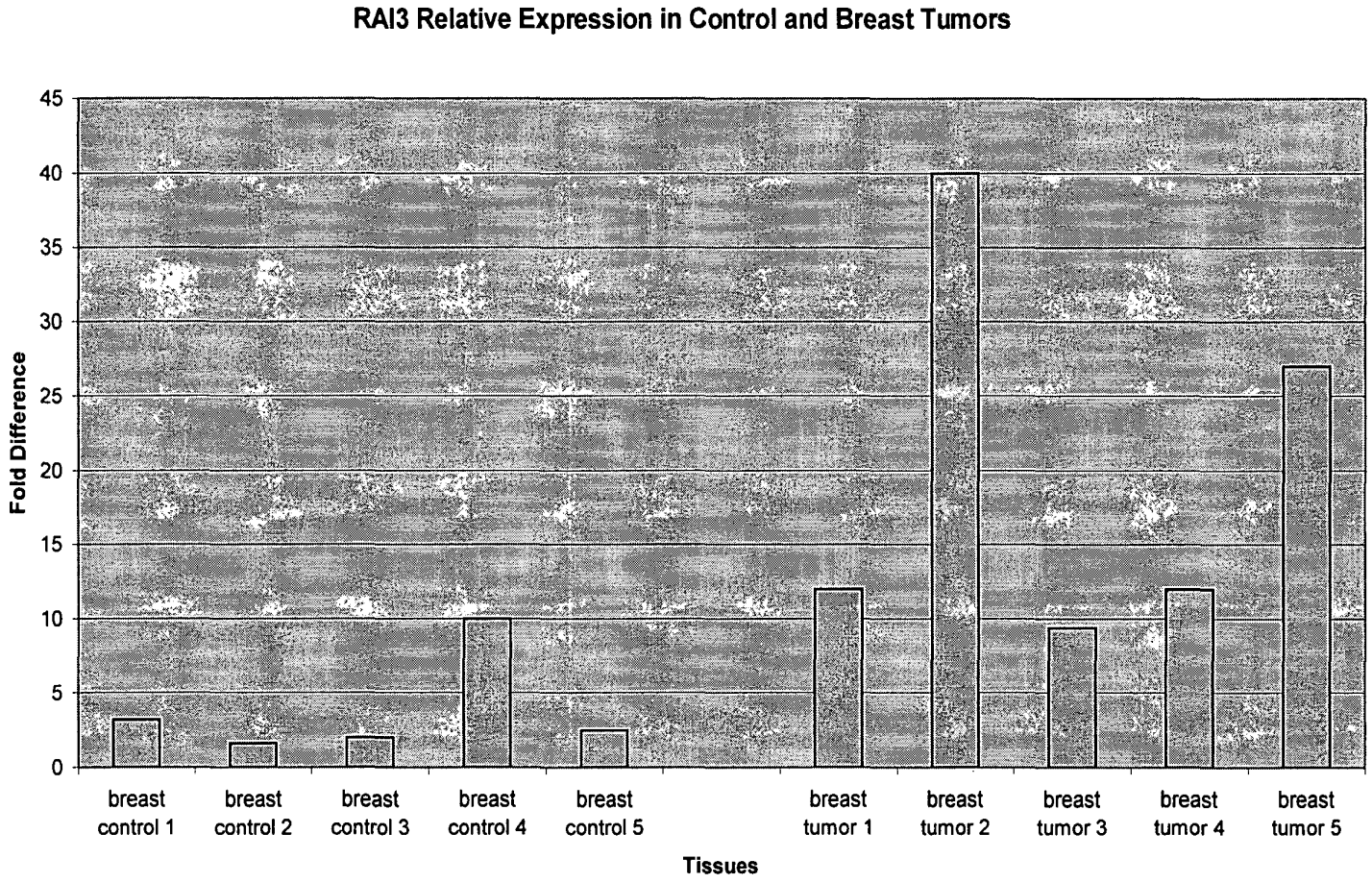

RAI3 Relative Expression in Control and Breast Tumors
Fold Difference
45
40
35
30
25
20
15
10
5
0
breast control 1
breast control 2
breast control 3
breast control 4
breast control 5
breast tumor 1
breast tumor 2
breast tumor 3
breast tumor 4
breast tumor 5
Tissues

FIG. 17

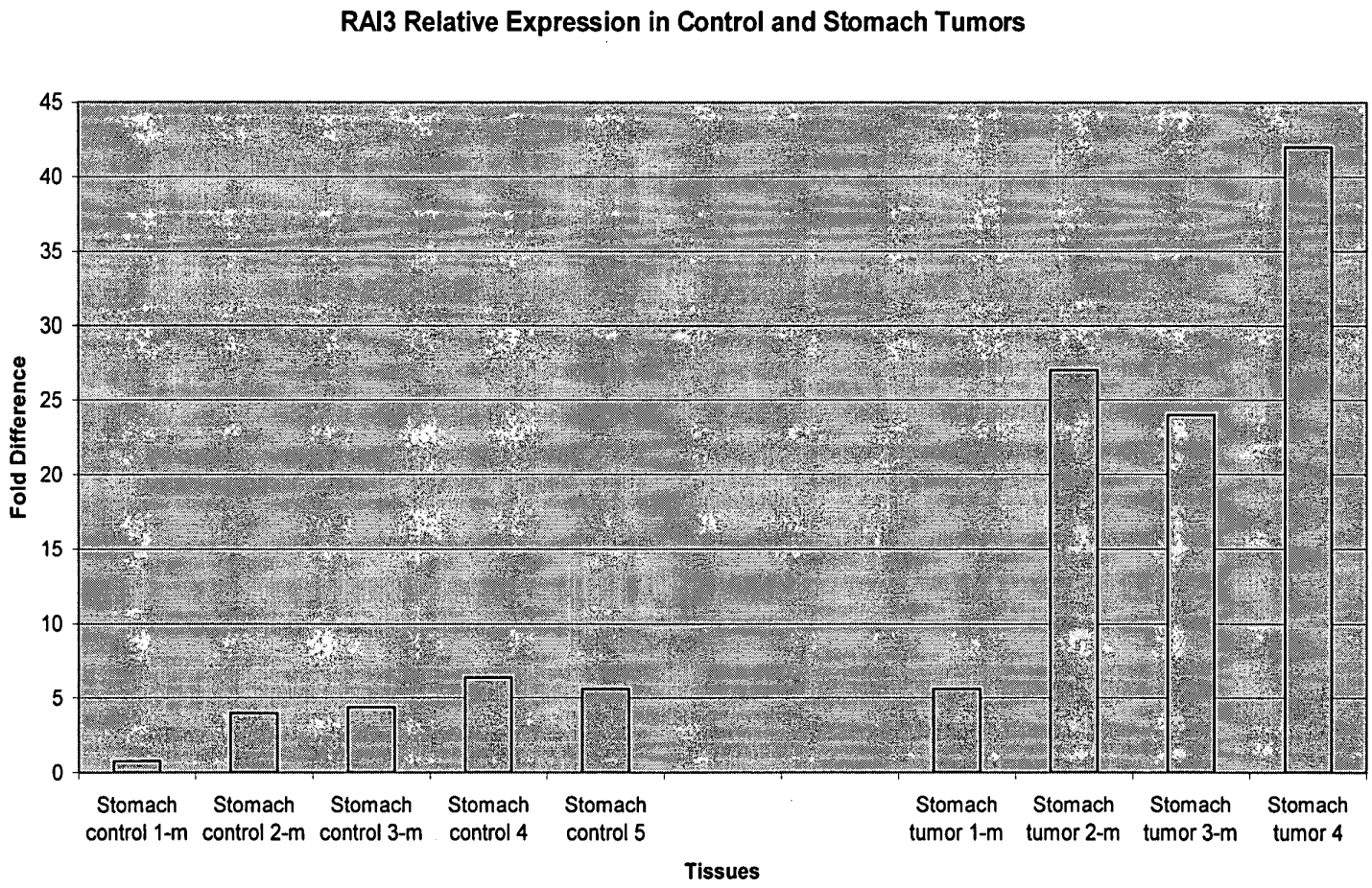

RAI3 Relative Expression in Control and Stomach Tumors
Fold Difference
45
40
35
30
25
20
15
10
5
0
Stomach control 1-m
Stomach control 2-m
Stomach control 3-m
Stomach control 4
Stomach control 5
Stomach tumor 1-m
Stomach tumor 2-m
Stomach tumor 3-m
Stomach tumor 4
Tissues

FIG. 18

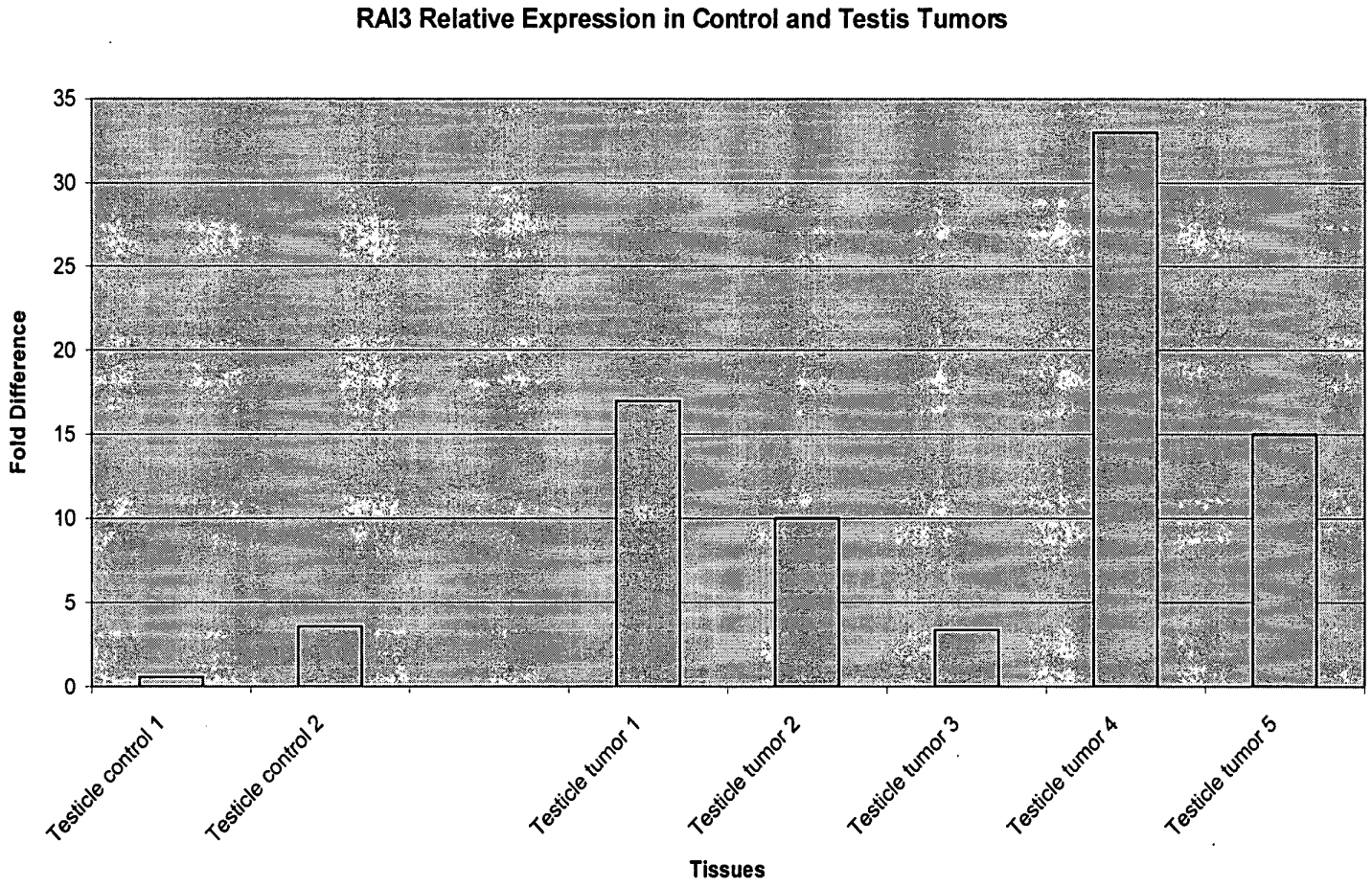

RAI3 Relative Expression in Control and Testis Tumors
Fold Difference
35
30
25
20
15
10
5
0
Testicle control 1
Testicle control 2
Testicle tumor 1
Testicle tumor 2
Testicle tumor 3
Testicle tumor 4
Testicle tumor 5
Tissues

FIG. 19A

```
GPCR5D_HUMAN NQQTAPVRYFLFGVLFALCFSCLLAHASNLVKLVRGCVSFSWTTILCIAIGCSLLQIII
GPCR5D_MOUSE NHQTAPVRYFLFGVLFAICFSCLLAHASNLVKLVRGRVSFCWTTILFIAIGVSLLQTII
RAI3_HUMAN   DGSTGPTRFFLFGILFSICFSCLLAHAVSLTKLVRGRKPLSLLVILGLAVGFSLVQDVI
RAI3_MOUSE   DGATGPTRFFLFGVLFAICFSCLLAHAFNLIKLVRGRKPLSWLVILSLAVGFSLVQDVI
RAI3_RAT     DRATGPTRFFLFGVLFALCFSCLLAHAFNLIKLVRGRKPLSWLVILSLAVGFSLVQDVI
RAI3_COW     NGGTGPTRFFLFGVLFALCFSCLLVHAFNLTKLVRGRQPLSMLVMLGLALGFSLVQDII
RAI3_HUMAN   DGSTGPTRFFLFGILFSICFSCLLAHAVGLTKLVRGRKPLSLLVILGLAVGFSLVQDVI
(w/SNP S/G)
```

FIG. 19B

```
GPCR5D_HUMAN RDSDGAEE..DVALTSYGTPIQPQTVDPTQECFIPQAKLSPQQDAGGV~~~~~~~~~~~~
GPCR5D_MOUSE C~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
RAI3_HUMAN   EITQGFEETGDTLYAPYSTHFQLQNQPPQKEFSIPRAHAWPSPYKDYEVKKEGS~~~~~~
RAI3_MOUSE   EITQGL.EMGDTLYAPYSTHFQLQNH..QKDFSIPRAQAPASPYNDYEGRKGDS
RAI3_HUMAN   EITRGFEETGDTLYAPYSTHFQLQNQPPQKEFSIPRAHAWPSPYKDYEVKKEGS~~~~~~
(w/SNP Q/R)
```

FIG. 20

```
HUMAN:  6    PDGCRNGLKSKYYRLCDKAEAWGIVLETVATAGVVTSVAFMLTLPILVCKVQDSNRRKML 65
             P GCR+ L S+Y+RLCD AE WGI LET A  G V  VA M  L  L+CKVQDSN+RKML
MOUSE:  124  PSGCRSDLDSRYHRLCDLAEGWGIALETLAAVGAVATVACMFALVFLICKVQDSNKRKML 303

                                                                  S
HUMAN:  66   PTQFLFLLGVLGIFGLTFAFIIGLDGSTGPTRFFLFGILFSICFSCLLAHAVSLTKLVRG 125
             P QFLFLLGVLG+FGLTFAFII LDG+TGPTRFFLFG+LF+ICFSCLLAHA +L KLVRG
MOUSE:  304  PAQFLFLLGVLGVFGLTFAFIIKLDGATGPTRFFLFGVLFAICFSCLLAHAFNLIKLVRG 483

                                                                  A
HUMAN:  126  RKPLSLLVILGLAVGFSLVQDVIAIEYIVLTMNRTNVNVFSELSAPRRNEDFVLLLTYVL 185
             RKPLS LVIL LAVGFSLVQDVIAIEY+VLTMNRTNVNVFSEL APRRNEDFV+LL YVL
MOUSE:  484  RKPLSWLVILSLAVGFSLVQDVIAIEYLVLTMNRTNVNVFSELPAPRRNEDFVMLLIYVL 663

HUMAN:  186  FLMALTFLMSSFTFCGSFTGWKRHGAHIYLTMLLSIAIWVAWITLLMLPDFDRRWDDTIL 245
              LM LTF  S   FCGSF+GWKRHG HI  T  LSIAIWVAWI LL++PD DR+WDDTIL
MOUSE:  664  VLMVLTFFASFLVFCGSFSGWKRHGFHICFTSFLSIAIWVAWIVLLLIPDIDRKWDDTIL 843

HUMAN:  246  SSALAANGWVFLLAYVSPEFWLLTKQRNPMDYPVEDAFCKPQLVKKSYGVENRAYSQEEI 305
             S+AL ANGWVFL  Y+ PEF  L +QR+P DYPVEDAFCKPQL+K+SYGVENRAYSQEEI
MOUSE:  844  STALVANGWVFLAFYILPEFRQLPRQRSPTDYPVEDAFCKPQLMKQSYGVENRAYSQEEI 1023

             R
HUMAN:  306  TQGFEETGDTLYAPYSTHFQLQNQPPQKEFSIPRAHAWPSPYKDYEVKKEGS 357
             TQG  E GDTLYAPYSTHFQLQN   QK+FSIPRA A  SPY DYE +K  S
MOUSE:  1024 TQGL-EMGDTLYAPYSTHFQLQNH--QKDFSIPRAQAPASPYNDYEGRKGDS 1170
```

FIG. 21

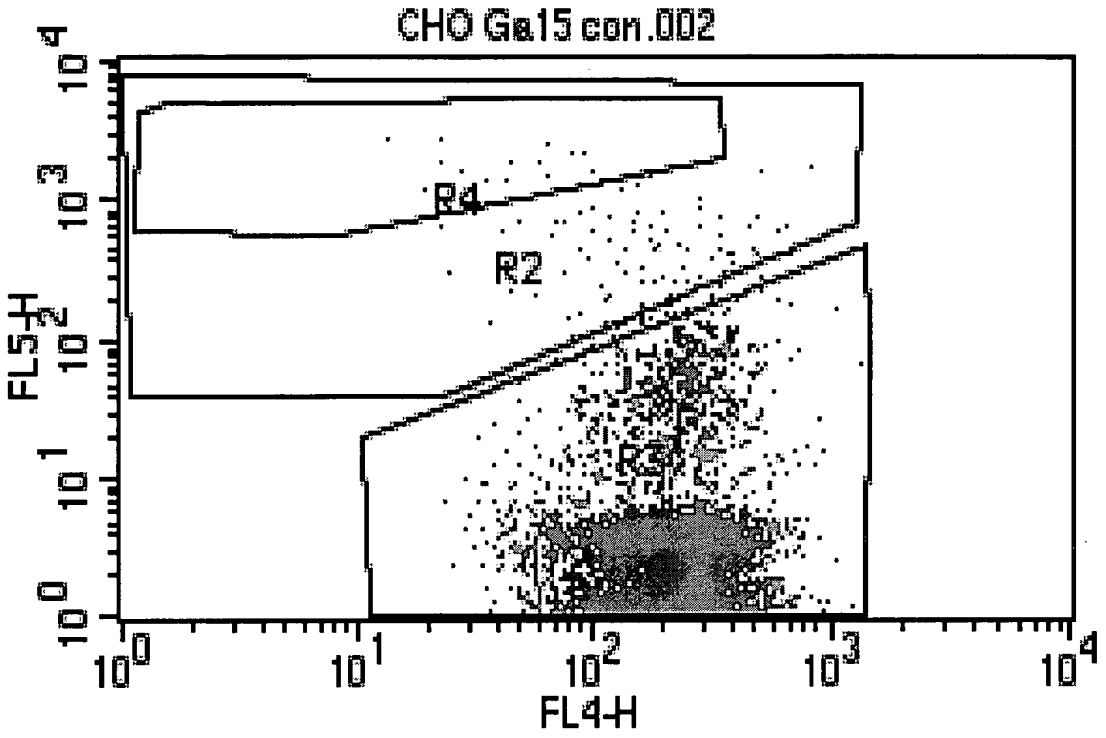


FIG. 22

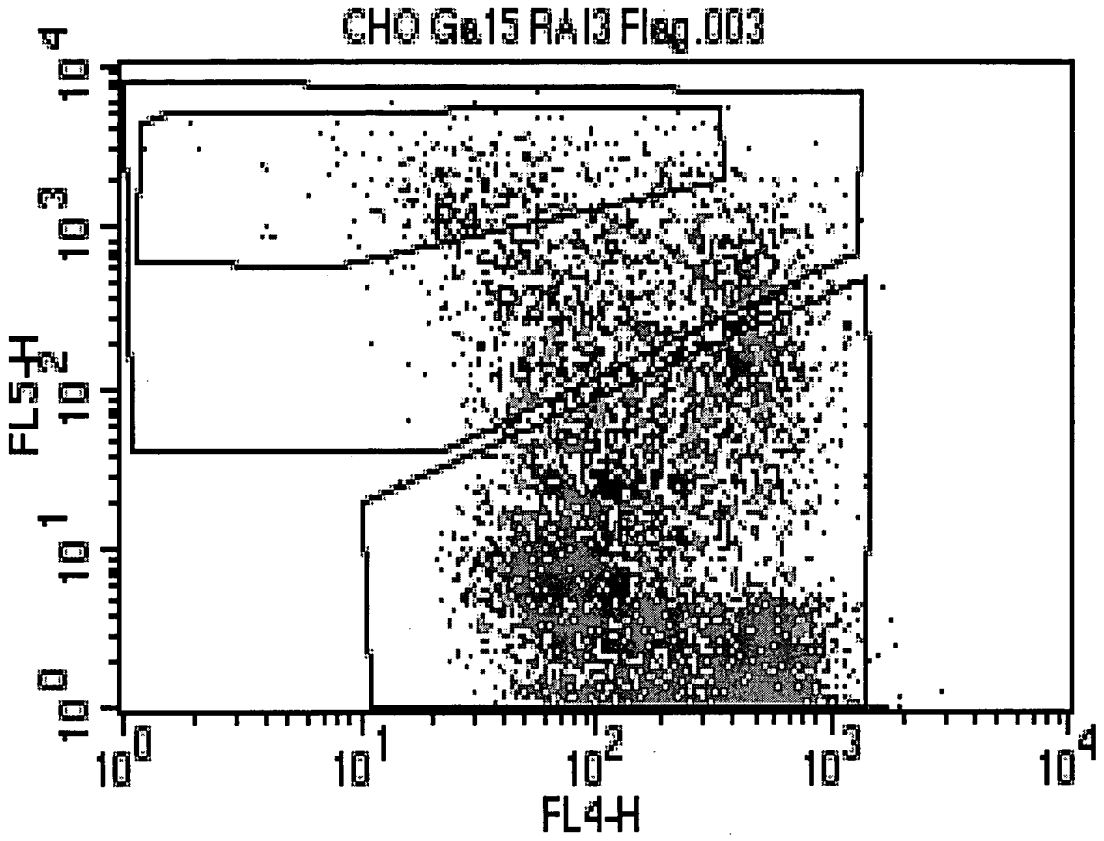


FIG. 23A

CHO NFAT Ga15 Control (Fluorescence)

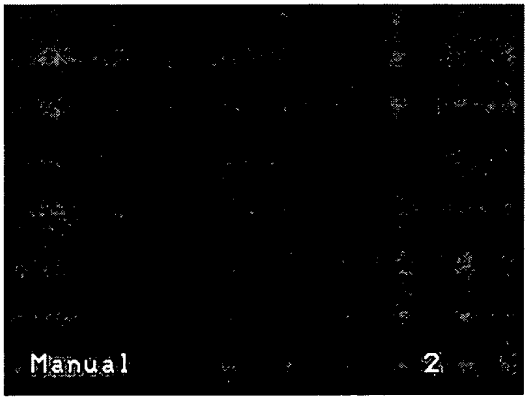


FIG. 23B

CHO NFAT Ga15 RAI-3 (Fluorescence)

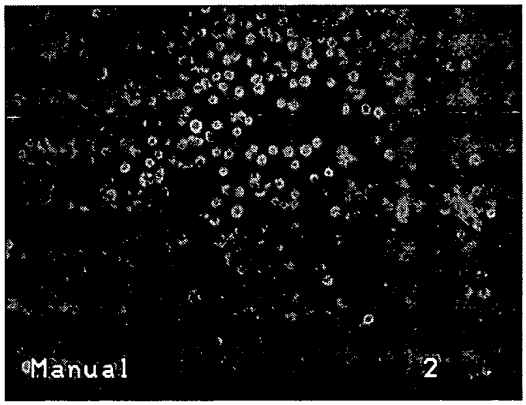


FIG. 24A

CHO NFAT Ga15

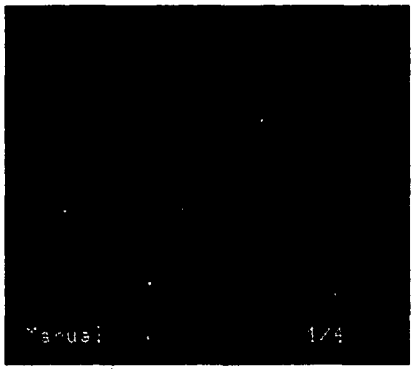


FIG. 24B

CHO NFAT Ga15 + T/P

FIG. 24C

CHO NFAT Ga15 oGPCR Intermediate

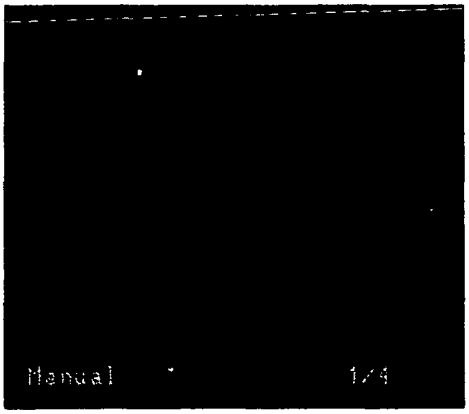


FIG. 24D

CHO NFAT Ga15 oGPCR High

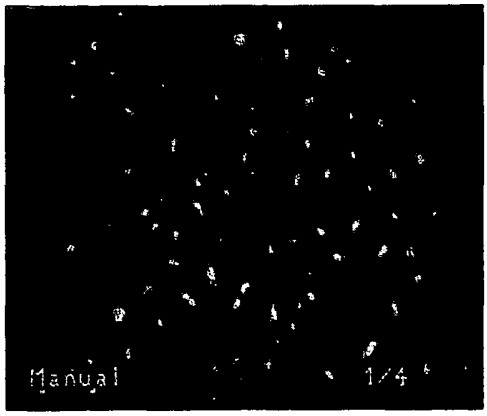


FIG. 25A

```
                .         .         .         .         .         .
  1  ataacagcatgaagtgccgtggaactggaataggcgtgtcctctccctcgaccctccccc   60

                .         .         .         .         .         .
 61  tccttgtccctctgctcacccctcgctcgttccctccctccggcgagggccncctttata   120

                .         .         .         .         .         .
121  acaactgctcagagtgcgagggcgggatagctgtccaaggtctcccccagcactgaggag   180

                .         .         .         .         .         .
181  ctcgcctgctgccctcttgcgcgcgggaagcagcaccaagttcacggccaacgccttggc   240

                .         .         .         .         .         .
241  actagggtccagaatggctacaacagtccctgatggttgccgcaatggcctgaaatccaa   300
  1                  M   A   T   T   V   P   D   G   C   R   N   G   L   K   S   K    16

                .         .         .         .         .         .
301  gtactacagactttgtgataaggctgaagcttggggcatcgtcctagaaacggtggccac   360
 17    Y   Y   R   L   C   D   K   A   E   A   W   G   I   V   L   E   T   V   A   T    36

                .         .         .         .         .         .
361  agcnggggttgtgacctcggtggccttcatgctcactctcccgatcctcgtctgcaaggt   420
 37    A   G   V   V   T   S   V   A   F   M   L   T   L   P   I   L   V   C   K   V    56

                .         .         .         .         .         .
421  gcaggactccaacaggcgaaaaatgctgcctactcagtttctcttcctcctgggtgtgtt   480
 57    Q   D   S   N   R   R   K   M   L   P   T   Q   F   L   F   L   L   G   V   L    76

                .         .         .         .         .         .
481  gggcatctttggcctcaccttcgccttcatnatcggactggangggagcacagggcccac   540
 77    G   I   F   G   L   T   F   A   F   I   I   G   L   D   G   S   T   G   P   T    96

                .         .         .         .         .         .
541  acgcttcttcctctttgggatcctcttttccatctgcttctcctgcctgctggctcatgc   600
 97    R   F   F   L   F   G   I   L   F   S   I   C   F   S   C   L   L   A   H   A   116

                .         .         .         .         .         .
601  tgtcngtctgaccaagctcgtccgggggaggaagccccttccctgttggtgattctggg   660
117    V   X   L   T   K   L   V   R   G   R   K   P   L   S   L   L   V   I   L   G   136

                .         .         .         .         .         .
661  tctggccgtgggcttcagcctagtccaggatgttatcgctattgaatatattgtcctgac   720
137    L   A   V   G   F   S   L   V   Q   D   V   I   A   I   E   Y   I   V   L   T   156

                .         .         .         .         .         .
721  catgaataggaccaacgtcaatgtcttttctgagctttccgctcctcgtcgcaatgaaga   780
157    M   N   R   T   N   V   N   V   F   S   E   L   S   A   P   R   R   N   E   D   176

                .         .         .         .         .         .
781  ctttgtcctcctgctcncctacgtcctcttcttgatggcgctgaccttcctcatgtcctc   840
177    F   V   L   L   L   X   Y   V   L   F   L   M   A   L   T   F   L   M   S   S   196
```

FIG. 25B

```
841  cttcaccttctgtggttccttcacgggctggaagagacatggggcccacatctacctcac   900
197   F  T  F  C  G  S  F  T  G  W  K  R  H  G  A  H  I  Y  L  T    216

901  gatgctcctctccattgccatctgggtggcctggatcaccctgctcatgcttcctgactt   960
217   M  L  L  S  I  A  I  W  V  A  W  I  T  L  L  M  L  P  D  F    236

961  tgaccgcaggtgggatgacaccatcctcagctccgccttggctgccaatggctgggtgtt   1020
237   D  R  R  W  D  D  T  I  L  S  S  A  L  A  A  N  G  W  V  F    256

1021 cctgttggcttatgttagtcccgagttttggctgctcacaaagcaacgaaaccccatgga   1080
257   L  L  A  Y  V  S  P  E  F  W  L  L  T  K  Q  R  N  P  M  D    276

1081 ttatcctgttgaggatgctttctgtaaaccncaactcgtgaagaagagctatggtgtgga   1140
277   Y  P  V  E  D  A  F  C  K  P  Q  L  V  K  K  S  Y  G  V  E    296

1141 gaacagagcctactctcaagaggaaatcactcnaggttttgaagagacaggggacacgct   1200
297   N  R  A  Y  S  Q  E  E  I  T  X  G  F  E  E  T  G  D  T  L    316

1201 ctatgccccctattccacacattttcagctgcagaaccagcctccccaaaaggaattctc   1260
317   Y  A  P  Y  S  T  H  F  Q  L  Q  N  Q  P  P  Q  K  E  F  S    336

1261 catcccacgggcccacgcttggccgagcccttacaaagactatgaagtaaagaaagaggg   1320
337   I  P  R  A  H  A  W  P  S  P  Y  K  D  Y  E  V  K  K  E  G    356

1321 cagctaactctgtcctgaagagtgggacaaatgcagccgggcggcagatctagcgggagc   1380
357   S                                                             357

1381 tcaaagggatgtgggcgaaatcttgagtcttctgagaaaactgtacaagacactacggga   1440

1441 acagtttgcctccctcccagcctcaaccacaattcttccatgctggggctgatgtgggct   1500

1501 agtaagactccagttcttagaggcgctgtagtatttttttttttttgtctcatcctttgg   1560

1561 atacttcttttaagtgggagtctcaggcaactcaagtttagacccttactctttttgttt   1620

1621 gtttttgaaacaggatcttgctctgtcacccaggcttgagtgcagtggtgcgatcacag   1680
```

FIG. 25C

```
1681  cccagtgcagcctcgaccacctgtgctcaagcaatcctcccatctccatctcccaaagtg  1740

1741  ctgggatgacaggcgtgagccacagctcccagcctaggcccttaatcttgctgttatttt  1800

1801  ccatggactaaaggtctggtcatctgagctcacgctggctcacacagctctaggggcctg  1860

1861  ctcctctaactcacagtgggttttgtgaggctctgtggcccagagcagacctgcatatct  1920

1921  gagcaaaaatagcaaaagcctctctcagcccactggcctgaatctacactggaagccaac  1980

1981  ttgctggcacccccgctccccaacccttcttgcctgggtaggagaggctaaagatcaccc  2040

2041  taaatttactcatctctctagtgctgcctcacattgggcctcagcagctccccagcacca  2100

2101  attcacaggtcacccctctcttcttgcactgtccccaaacttgctgtcaattccgagatc  2160

2161  taatctccccctacgctctgccaggaattctttcagacctcactagcacaagcccggttg  2220

2221  ctccttgtcaggagaatttgtagatcattctcacttcaaattcctggggctgatacttct  2280

2281  ctcatcttgcaccccaacctctgtaaatagatttaccgcatttacggctgcattctgtaa  2340

2341  gtgggcatggtctcctaatggaggagtgttcattgtataataagttattcacctgagtat  2400

2401  gcaataaagatgtggtggccactctttcatggtggtggcagcaaaaaaaaaaaaaa  2456
```

FIG. 26A

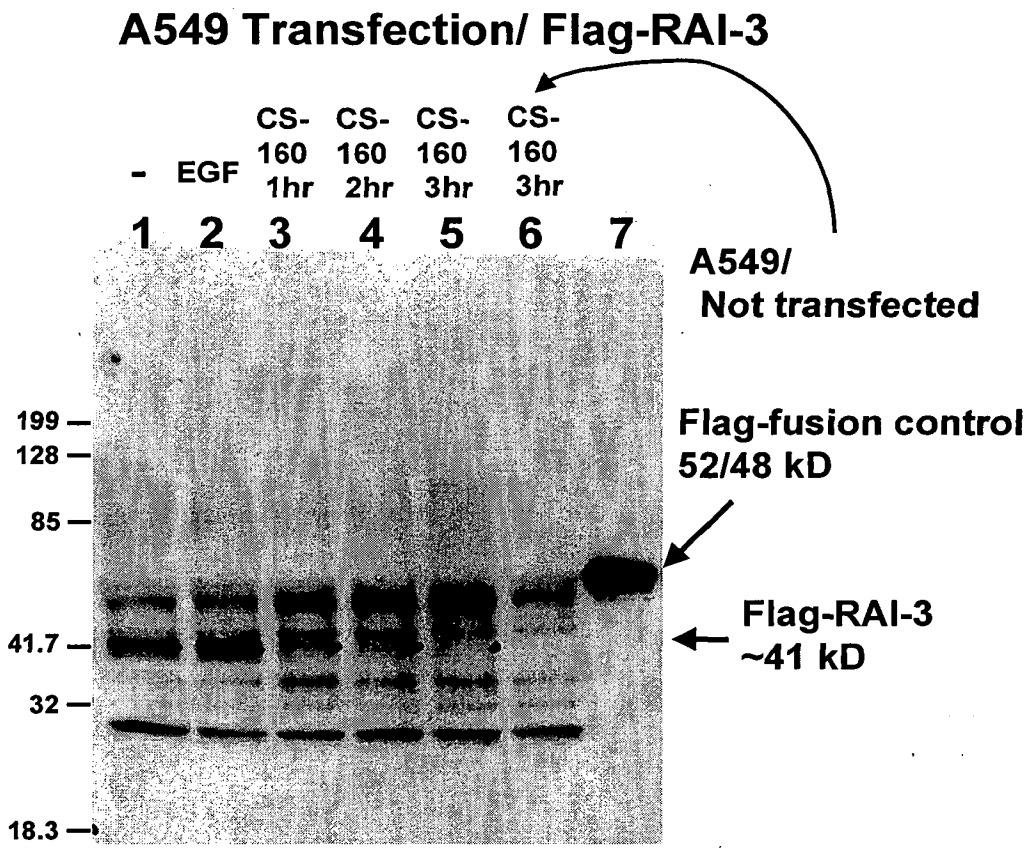

A549 Transfection/ Flag-RAI-3
-
EGF
CS-160 1hr
CS-160 2hr
CS-160 3hr
CS-160 3hr
1 2 3 4 5 6 7
A549/ Not transfected
199
128
85
41.7
32
18.3
Flag-fusion control 52/48 kD
Flag-RAI-3 ~41 kD

FIG. 26B

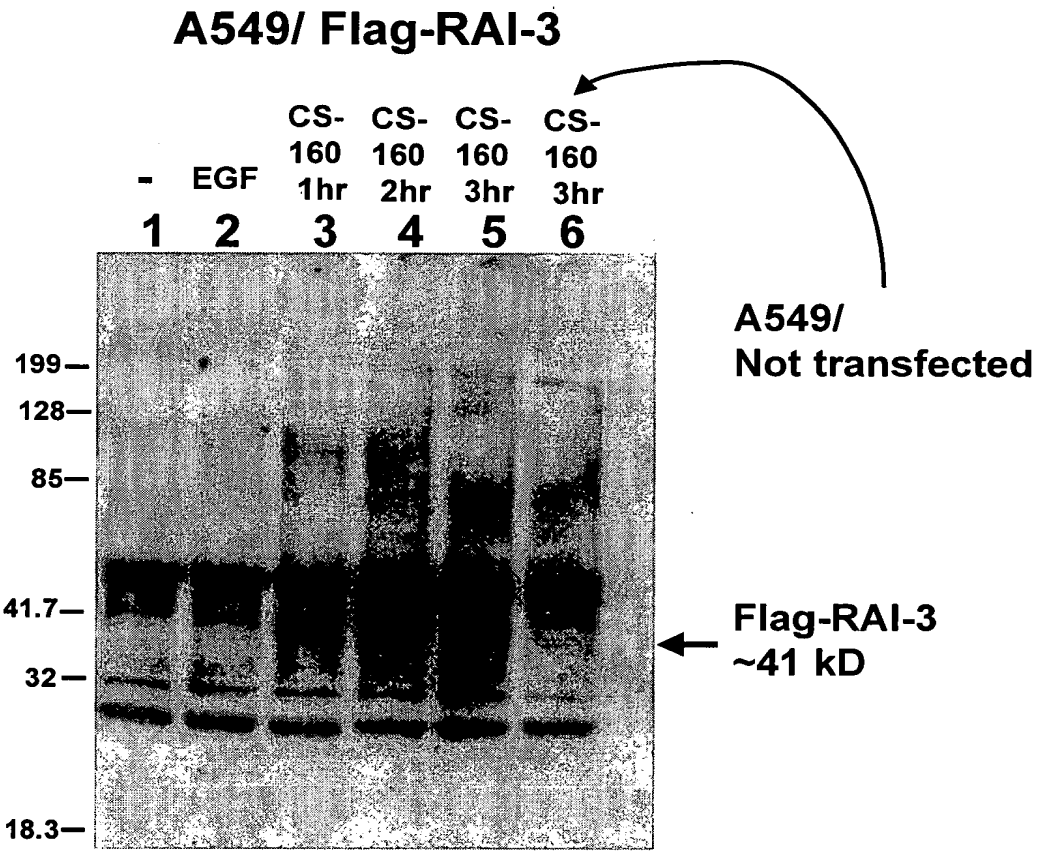

A549/ Flag-RAI-3
-
EGF
CS-160 1hr
CS-160 2hr
CS-160 3hr
CS-160 3hr
1
2
3
4
5
6
199
128
85
41.7
32
18.3
A549/
Not transfected
Flag-RAI-3
~41 kD

FIG. 27A

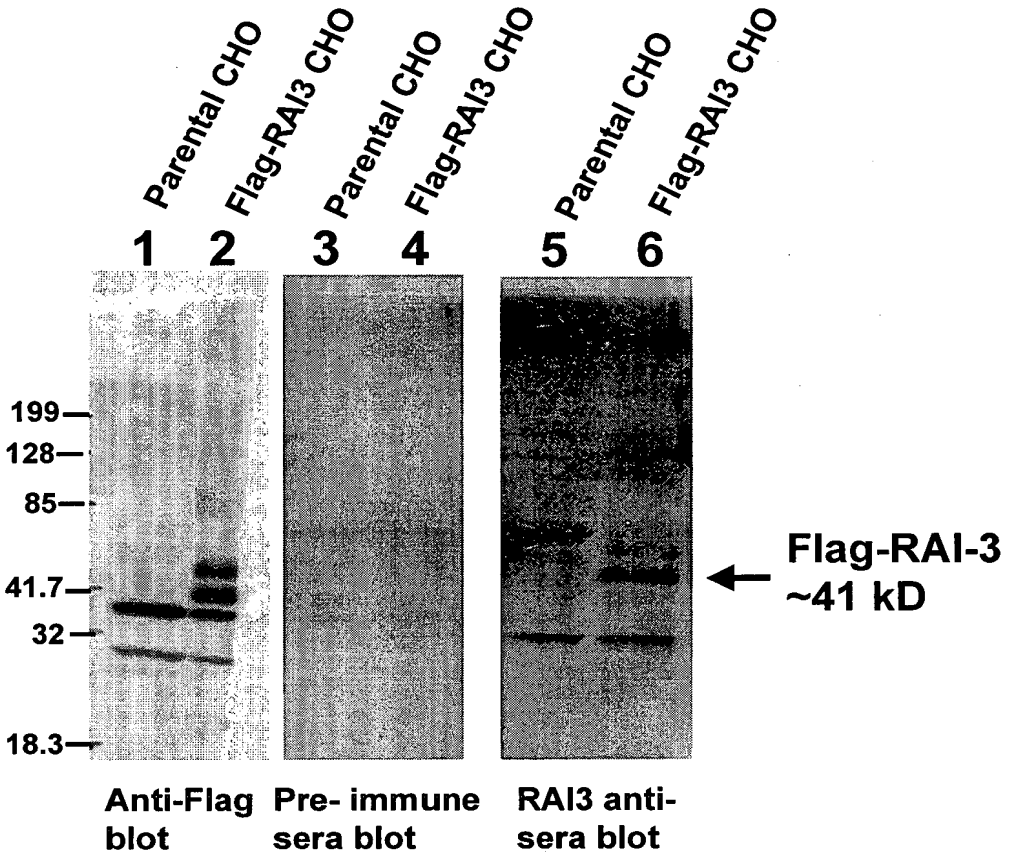

Parental CHO
Flag-RAI3 CHO
Parental CHO
Flag-RAI3 CHO
Parental CHO
Flag-RAI3 CHO
1
2
3
4
5
6
199
128
85
41.7
32
18.3
Flag-RAI-3
~41 kD
Anti-Flag blot
Pre- immune sera blot
RAI3 anti-sera blot

FIG. 27B

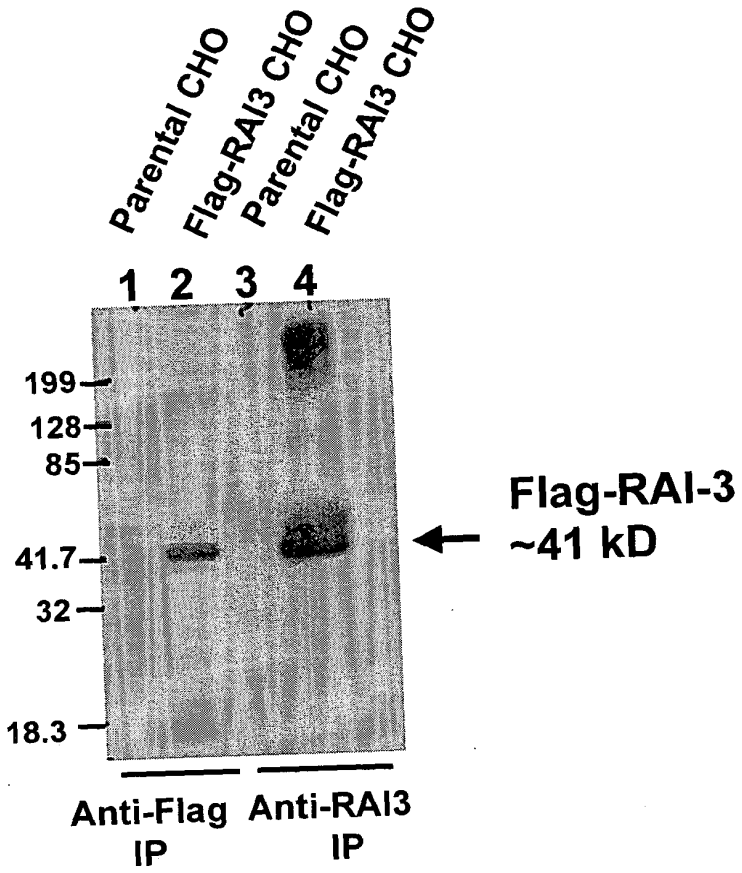

Parental CHO
Flag-RAI3 CHO
Parental CHO
Flag-RAI3 CHO
1 2 3 4
199
128
85
41.7
32
18.3
Flag-RAI-3
~41 kD
Anti-Flag IP
Anti-RAI3 IP

FIG. 28A

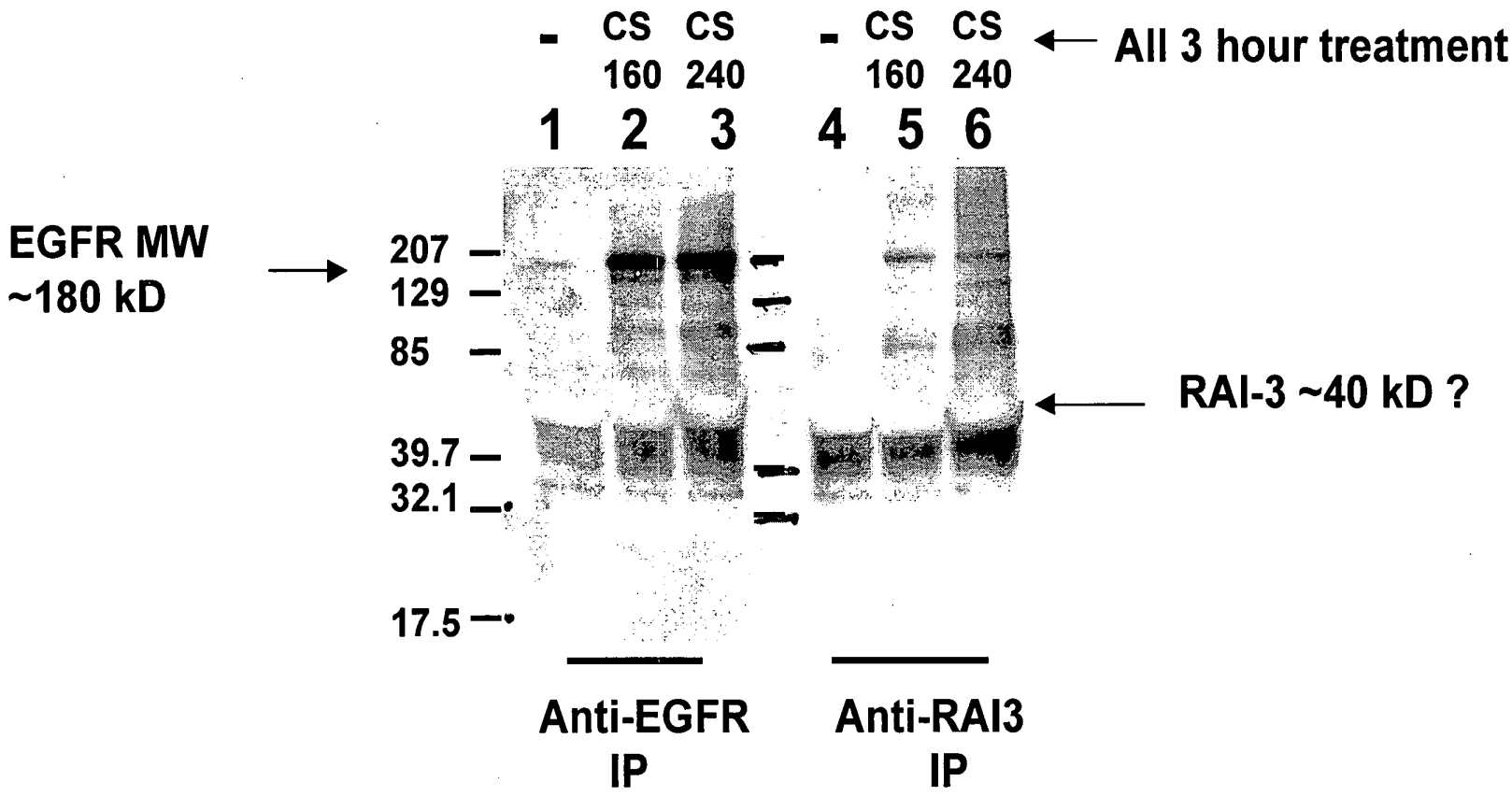

- CS 160 CS 240 - CS 160 CS 240
All 3 hour treatment
1 2 3 4 5 6
EGFR MW ~180 kD
207
129
85
39.7
32.1
17.5
RAI-3 ~40 kD ?
Anti-EGFR IP
Anti-RAI3 IP

FIG. 28B

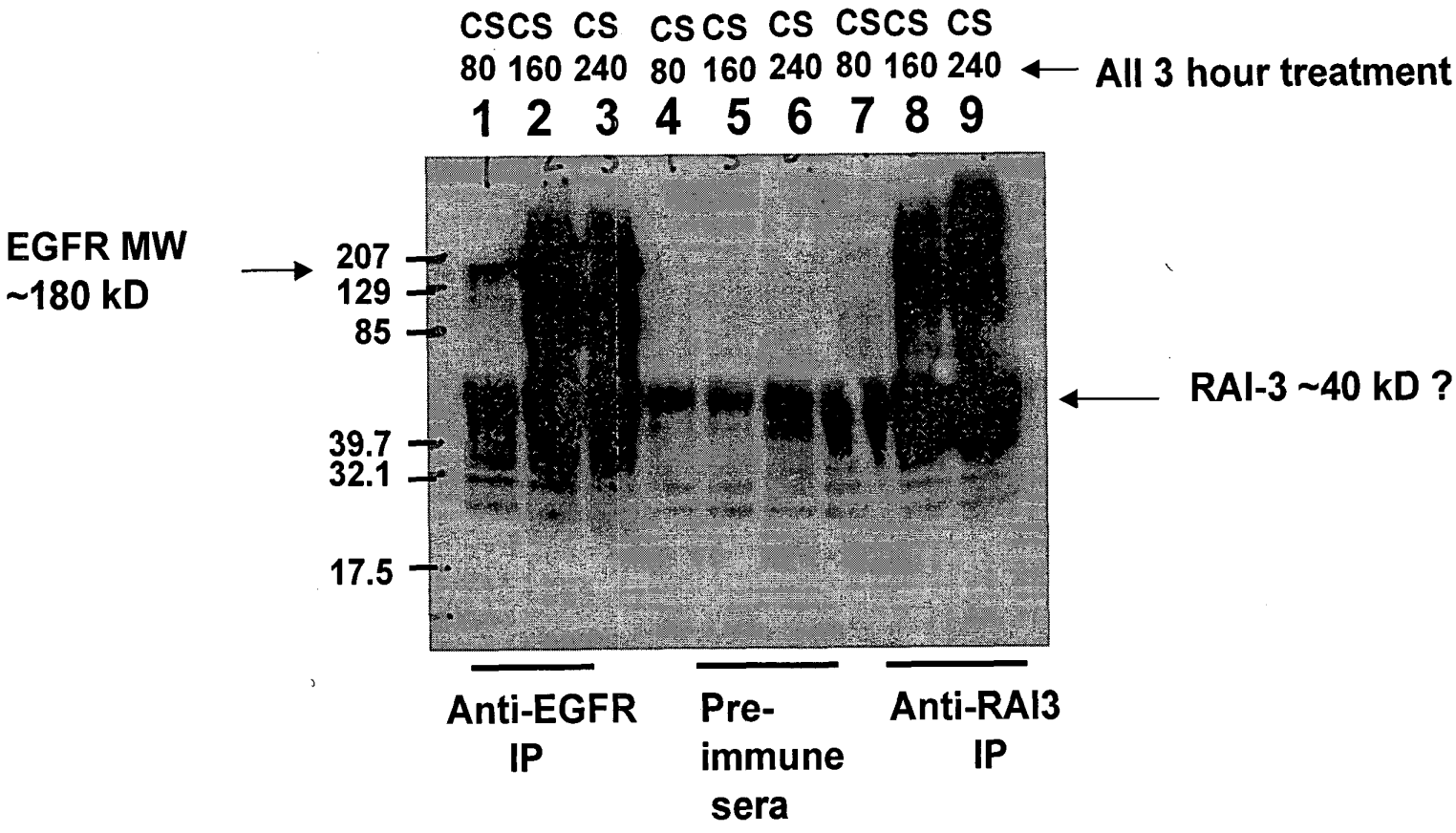
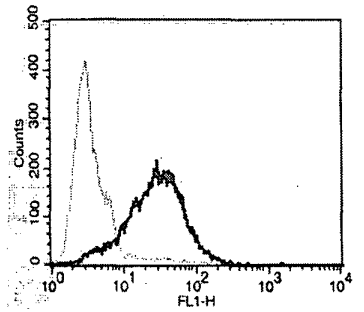
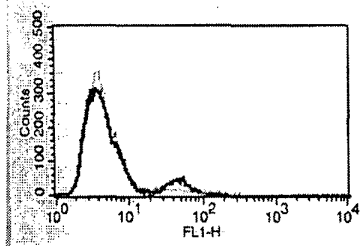

CSCS CS CS CS CS CSCS CS
80 160 240 80 160 240 80 160 240
1 2 3 4 5 6 7 8 9
All 3 hour treatment
EGFR MW
~180 kD
207
129
85
39.7
32.1
17.5
RAI-3 ~40 kD ?
Anti-EGFR IP
Pre-immune sera
Anti-RAI3 IP

FIG. 29



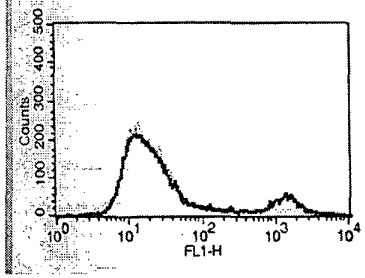
Anti- Flag

% Gated	Mean	
100.00	4.82	parental
100.00	34.97	*CHO/FlagRAI3 clone B8*



Rabbit anti-pre-immune

% Gated	Mean	
100.00	8.23	parental
100.00	9.19	*CHO/FlagRAI3 clone B8*



Rabbit Anti-RAI3

% Gated	Mean	
100.00	68.40	parental
100.00	193.51	*CHO/FlagRAI3 clone B8*

FIG. 30

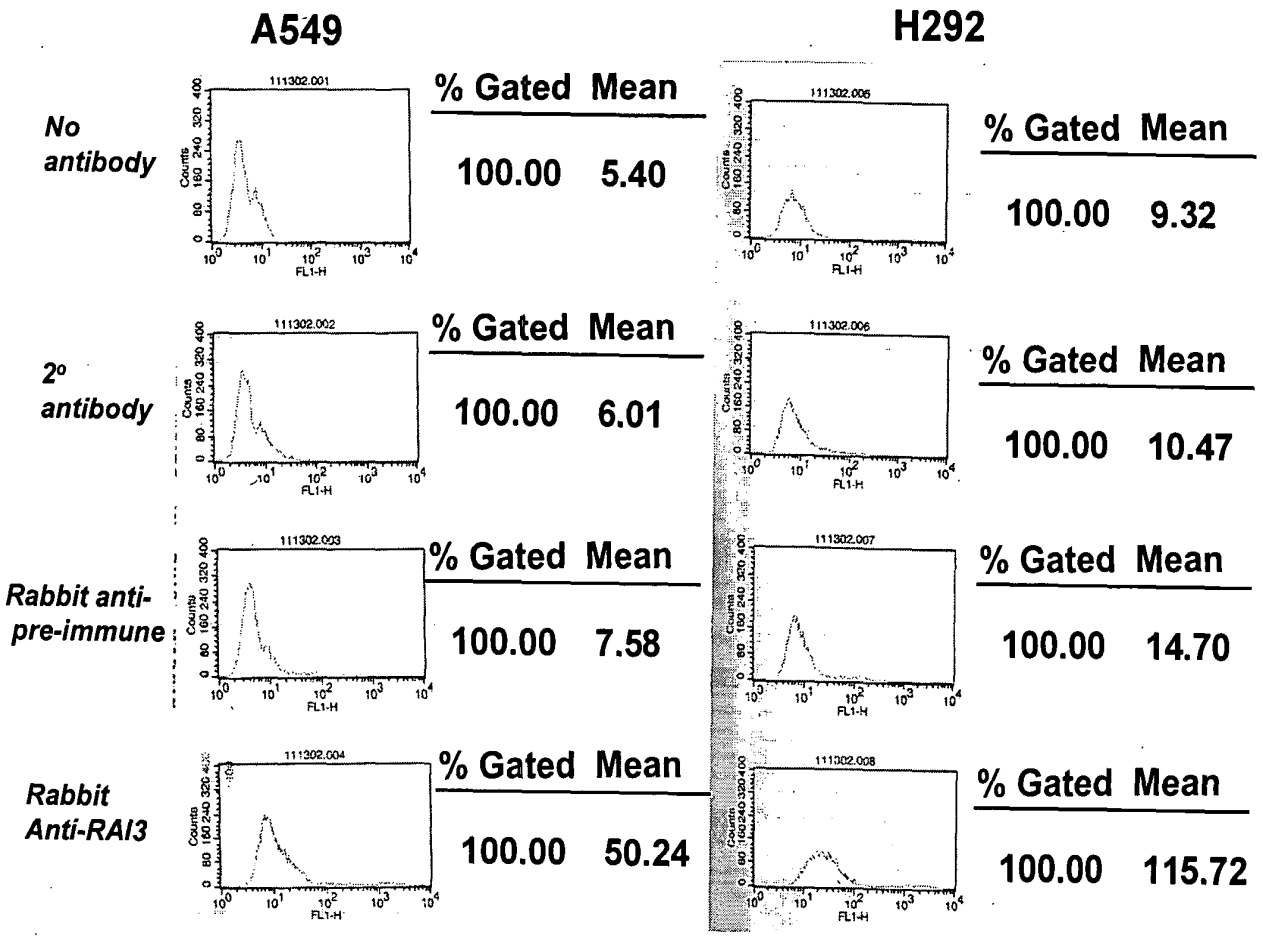

A549
H292
No antibody
2° antibody
Rabbit anti-pre-immune
Rabbit Anti-RAI3
% Gated Mean
100.00 5.40
100.00 9.32
100.00 6.01
100.00 10.47
100.00 7.58
100.00 14.70
100.00 50.24
100.00 115.72
111302.001
111302.002
111302.003
111302.004
111302.006
111302.006
111302.007
111302.008
Counts
FL1-H

FIG. 31

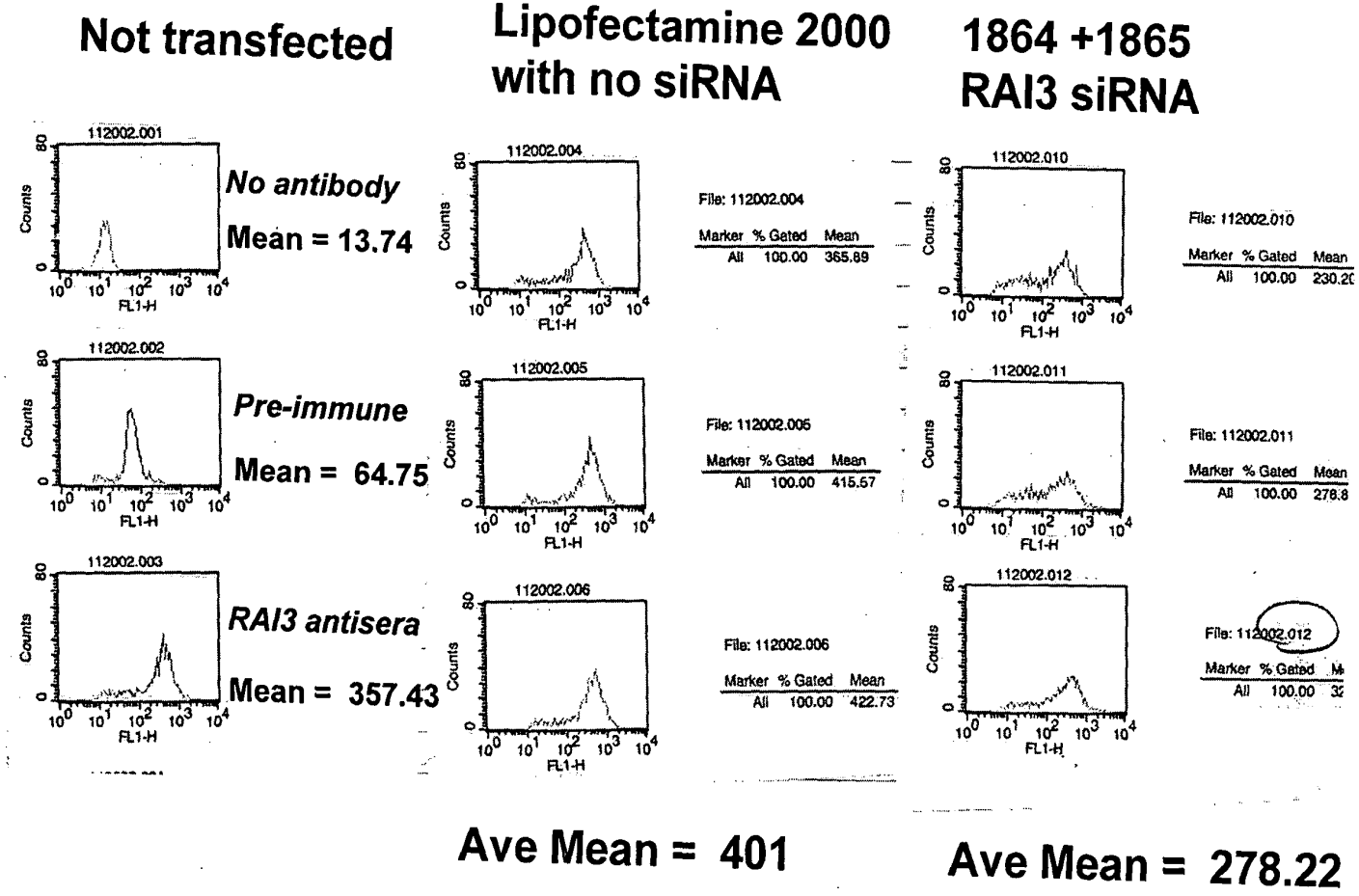
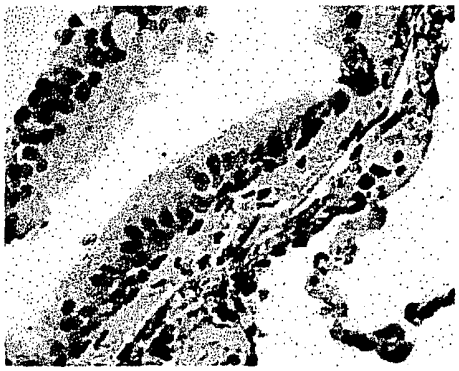

Not transfected
Lipofectamine 2000 with no siRNA
1864 +1865 RAI3 siRNA
112002.001
No antibody
Mean = 13.74
112002.002
Pre-immune
Mean = 64.75
112002.003
RAI3 antisera
Mean = 357.43
112002.004
File: 112002.004
Marker % Gated Mean
All 100.00 365.89
112002.005
File: 112002.005
Marker % Gated Mean
All 100.00 415.57
112002.006
File: 112002.006
Marker % Gated Mean
All 100.00 422.73
112002.010
File: 112002.010
Marker % Gated Mean
All 100.00 230.2
112002.011
File: 112002.011
Marker % Gated Mean
All 100.00 278.8
112002.012
File: 112002.012
Marker % Gated M
All 100.00 3
Counts
FL1-H
Ave Mean = 401
Ave Mean = 278.22

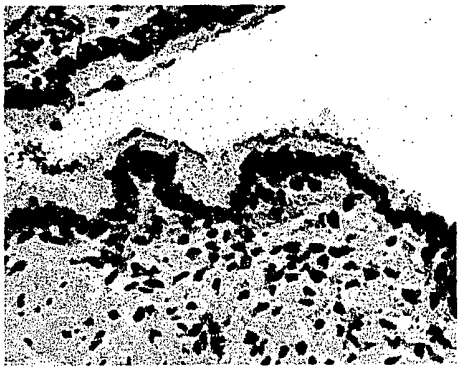
FIG. 33

A. Normal Lung Tissue



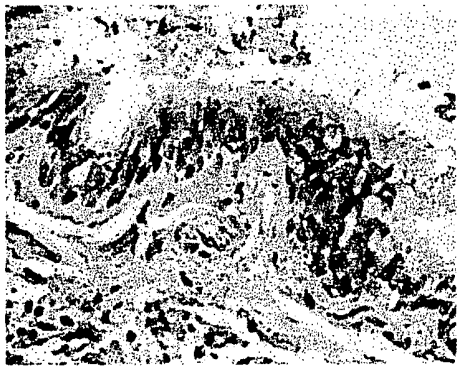
Respiratory Epithelium, Normal Lung

B. Normal Lung Tissue



Respiratory Epithelium, Normal Lung

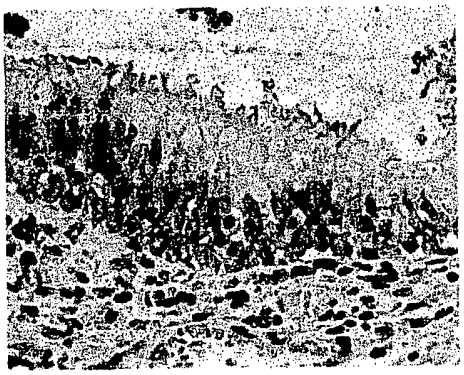
C. Emphysema, Human Lung Tissue



Respiratory Epithelium, Emphysema

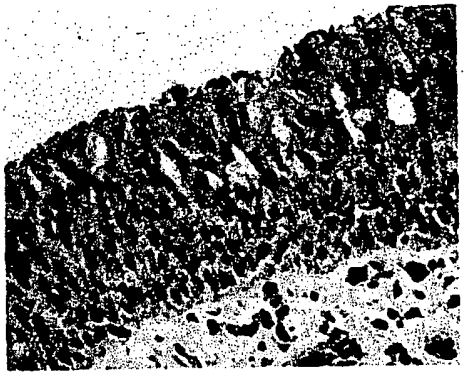
FIG. 34

A. Chronic Bronchitis, Human Lung Tissue



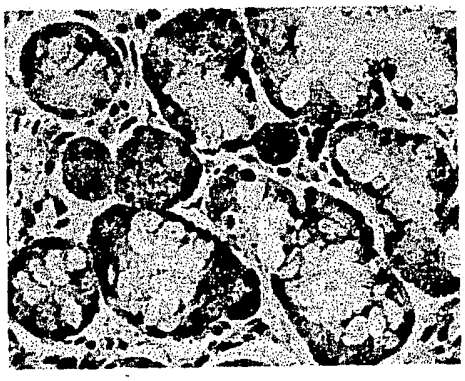
Respiratory Epithelium, Bronchitis

B. Chronic Bronchitis, Human Lung Tissu



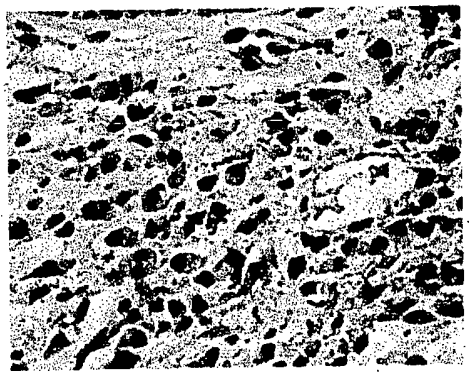
Respiratory Epithelium, Bronchitis

C. Chronic Bronchitis, Human Lung Tissue



Seromucous Glands, Bronchitis

D. Chronic Bronchitis, Human Lung Tissu



Mucosal Inflammation, Bronchitis

FIG. 32

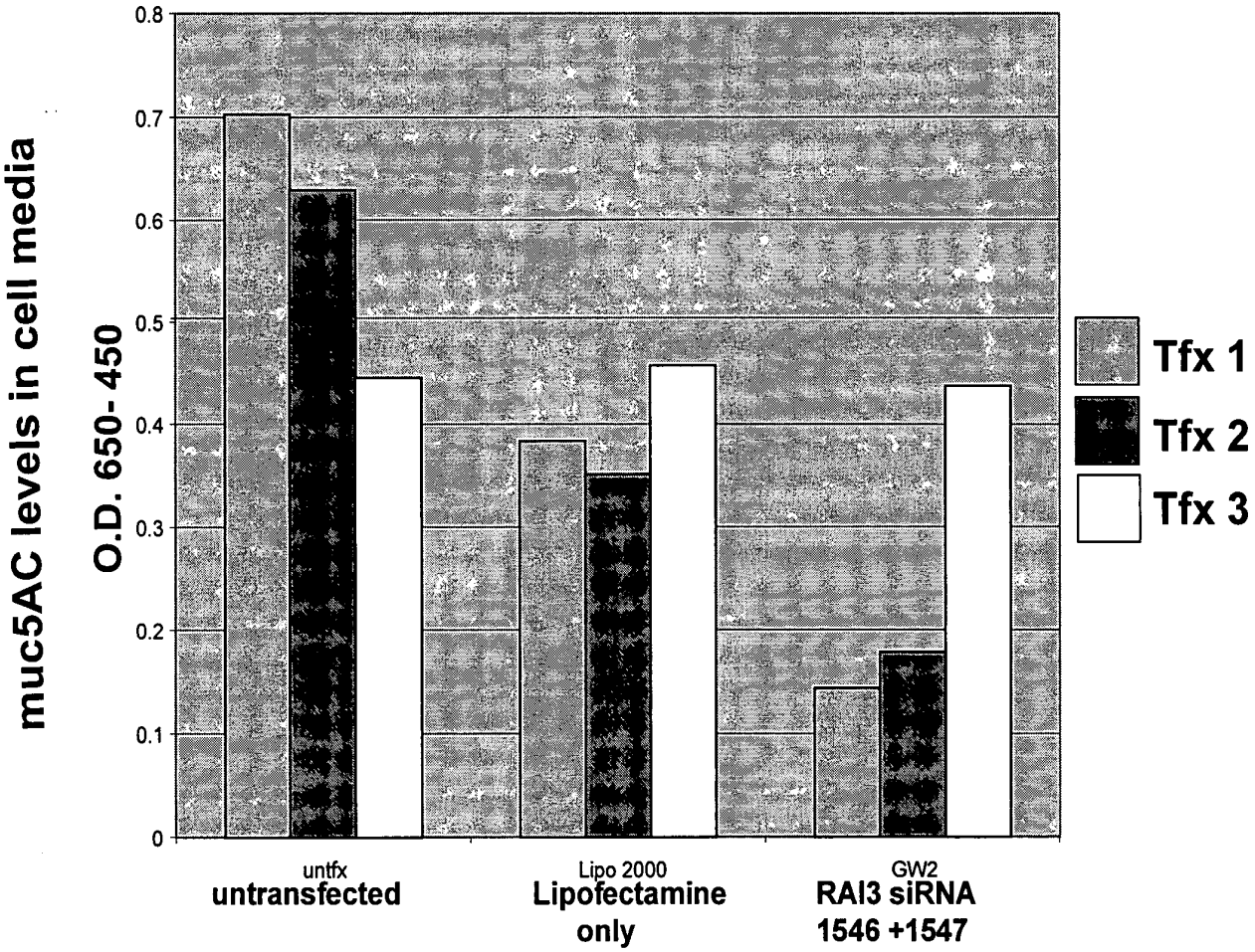
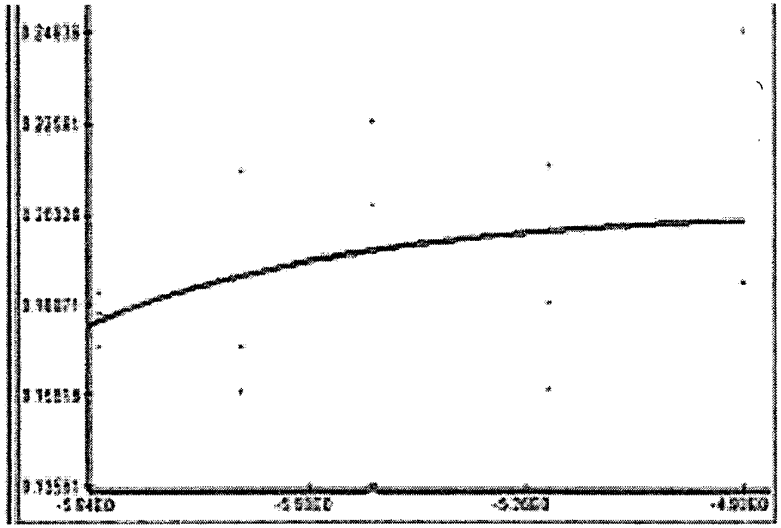

muc5AC levels in cell media
O.D. 650- 450
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
untfx
untransfected
Lipo 2000
Lipofectamine only
GW2
RAI3 siRNA 1546 +1547
Tfx 1
Tfx 2
Tfx 3

FIG. 35

A.



B.